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OM protein - protein search, using sw model
Run on: March 1, 2004, 16:36:28 ; Search time 54 Seconds
(without alignments)
596.489 Million cell updates/sec

Title: US-10-062-599-59
Perfect score: 608
Sequence: 1 MARGSLRLRLVLGLWLA.....LSGFLVWRRCRRERSPPXP 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseqp29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	99.8	114	2 AAW73409	Human sec
2	571	93.9	129	2 AAW88506	Human liv
3	571	93.9	129	3 AAY57940	Human tra
4	571	93.9	129	3 AAU03498	Human TWE
5	571	93.9	129	5 ABP61512	Human NF-
6	571	93.9	129	5 AAU79827	Human typ
7	571	93.9	129	6 ADA56889	Human sec
8	571	93.9	129	6 ABUS6716	lung canc
9	571	93.9	129	7 ADC74112	Human sec
10	571	93.9	129	7 ADD37867	Human sec
11	571	93.9	129	7 ADD89033	TAT274.1
12	450	74.0	129	5 AAU79828	Mouse typ
13	433	71.2	309	4 AAU03500	Human sec
14	274.5	45.1	112	3 AAY91463	Human sec
15	274.5	45.1	112	6 ADA57390	Human sec
16	274.5	45.1	112	7 ADC74462	Human sec
17	274.5	45.1	112	7 ADD38025	Human sec
18	274.5	45.1	155	3 AAY91604	Human sec
19	274.5	45.1	155	6 ADA57391	Human sec
20	274.5	45.1	155	7 ADD37391	Human sec
21	274.5	45.1	155	7 ADC74463	Human sec
22	274.5	45.1	155	7 ADD38026	Human sec
23	191	31.0	32	3 AAY91552	Human sec
24	97.5	16.0	171	7 ADA49370	Human Fnl
25	97.5	16.0	171	7 ADB90668	TALL-1R g
			171	7 ADB90665	TALL-1R g

26	97.5	16.0	185	7 ADB90663	TALL-1R g
27	97	16.0	170	7 ADB90667	TALL-1R g
28	96.5	15.9	186	7 ADB90675	TALL-1R p
29	94.5	15.5	185	5 AAE22269	Human BAF
30	92.5	15.2	185	5 AAE22267	Human BAF
31	92.5	15.2	185	5 AAE22266	Human BAF
32	91.5	15.0	185	5 AAE22270	Human BAF
33	91.5	15.0	185	5 AAE22271	Human BAF
34	89.5	14.7	185	5 AAE22268	Human BAF
35	88.5	14.6	185	5 AAE22242	Human mac
36	88.5	14.6	1307	7 AAE39374	Human CRU
37	88.5	14.6	1388	5 ABP70118	Human NOV
38	88.5	14.6	1388	5 ABP70117	Human NOV
39	87.5	14.4	185	7 ABR82287	Human BRO
40	87	14.3	184	5 ABB81483	Human Ztn
41	87	14.3	184	6 AAE35227	Human Ztn
42	87	14.3	184	6 ADA49363	Human BAF
43	87	14.3	184	6 ABP7721	Amino aci
44	87	14.3	184	6 ABR61767	Human PRO
45	87	14.3	266	5 AAE22243	Human JST

ALIGNMENTS

RESULT 1

AAW73409

ID AAW73409 standard; protein; 114 AA.

XX AC AAW73409;

XX XX 19-FEB-1999 (first entry)

XX DT Human secreted protein encoded by Gene No. 13.

XX DB

XX KW Secreted protein; human; protein therapy; gene therapy; blood disorder;
XX KW pathological condition; diagnosis; cancer; neurological disorder;
XX KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
XX KW immune system disorder; Alzheimer's disease; cognitive disorder;
XX KW schizophrenia; prostate disease; autoimmune disorder; AIDS.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 114

XX FT /note= "unspecified amino acid"

XX PN WO9854206-Al.

XX XX 03-DEC-1998.

XX PD 28-MAY-1998; 98WO-US010868.

XX PF 30-MAY-1997; 97US-0044039P.

XX PR 30-MAY-1997; 97US-0048093P.

XX PR 30-MAY-1997; 97US-0048101P.

XX PR 30-MAY-1997; 97US-0048190P.

XX PR 30-MAY-1997; 97US-0050935P.

XX PR 30-MAY-1997; 97US-0056250P.

XX PR 29-AUG-1997; 97US-0056293P.

XX PR 29-AUG-1997; 97US-0056296P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PA Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;

XX PI Ni J, Feng P;

XX XX WPI; 1999-070209/06.

XX DR N-PSDB; AAV08823.

XX DR

XX DR

XX XX New isolated human genes - useful for diagnosis and treatment of, e.g.

XX FT cancers, neurological disorders, immune diseases, developmental disorders

XX FT

or blood disorders.

Claim 11; Page 153; 18pp; English.

This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic diseases, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners

Sequence 114 AA;

Query Match 99.8%; Score 607; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 1.3e-55;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

QY 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRSSPPP 113

DB 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRSSPPP 113

RESULT 2

AAW88506

ID AAW88506 standard; protein; 129 AA.

AC AAW88506;

XX 30-MAR-1999 (first entry)

XX Human liver clone HP10432-encoded membrane protein.

XX Transmembrane protein; HP10432; human; liver.

XX Homo sapiens.

XX WO9855508-A2.

XX 10-DEC-1998.

XX 03-JUN-1998; 98WO-JP002445.

XX 03-JUN-1997; 97JP-00144948.

XX (SAGA) SAGAMI CHEM RES CENTRE.

XX (PROT-) PROTEGENE INC.

XX Kato S, Sekine S, Yamaguchi T;

XX WPI; 1999-045730/04.

XX N-PSDB; AAW84374.

XX New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy.

XX Claim 1; Page 152-153; 178pp; English.

This is the amino acid sequence of a transmembrane protein encoded by human liver cDNA clone HP10432 (see AAW84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAW84359-76) coding for 18 transmembrane proteins (see AAW8491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines

Sequence 129 AA;

Query Match 93.9%; Score 571; DB 2; Length 129;

Best Local Similarity 94.7%; Pred. No. 8.4e-52;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

QY 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRSSPPP 113

DB 61 SDFCLGCAAAPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTP 113

RESULT 3

AAV57940

ID AAV57940 standard; protein; 129 AA.

XX AAV57940;

XX 23-MAR-2000 (first entry)

XX Human transmembrane protein HTMPN-64.

XX Human; transmembrane protein; HTMPN; diagnosis; immunospecific;

XX antiproliferative; neuroprotective; immune disorder;

XX reproductive disorder; smooth muscle disorder; neurological disorder;

XX gastrointestinal disorder; developmental disorder;

XX cell proliferative disorder.

XX Homo sapiens.

XX WO9961471-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011904.

XX 29-MAY-1998; 98US-0087260P.

XX 02-JUL-1998; 98US-0091674P.

XX 02-OCT-1998; 98US-0102954P.

XX 24-NOV-1998; 98US-0109869P.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;

XX Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;

XX WPI; 2000-072605/06.

XX N-PSDB; AAZ56761.

XX Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders.

XX Claim 1; Page 163; 229pp; English.

XX AAZ56698 to AAZ56776 encode AAV57877 to AAV57955 which represent human

CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The
CC transmembrane protein have immunospecific, antiproliferative and
CC neuroprotective activities. The human transmembrane proteins,
CC polynucleotides encoding them and other compositions and methods from the
CC present invention, can be used for the diagnosis, treatment or prevention
CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,
CC developmental and cell proliferative disorders. The HTMPN's can be used
CC to treat or prevent disorders associated with a decreased expression or
CC activity of HTMPN

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 3; Length 129;
Best Local Similarity 94.7%; Pred. No. 8.4e-52;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
QY 61 SDFCLGCAAPAPPFRLLWPIILGALSILTFVLGLLGSFLVWRRRRSSPPPP 113
Db 61 SDFCLGCAAPAPPFRLLWPIILGALSILTFVLGLLGSFLVWRRRRREKFTTF 113

RESULT 4
AAU03498
ID AAU03498 standard; protein; 129 AA.

XX AAU03498;
XX 26-SEP-2001 (first entry)
XX Human TWEAK receptor (TWEAKR) polypeptide.

XX TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
KW rubellosis; uveitis; macular degeneration; arthritis; rheumatism;
KW corneal graft neovascularisation; psoriasis; tumour; haemophilic joint;
KW malignant tumour; sarcoma; carcinoma; benign tumour; wound granulation;
KW preneoplastic condition; myocardial angiogenesis; wound granulation;
KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;
KW peripheral atherosclerosis.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Domain 1..78
FT FT /note= "Extracellular domain"
FT Peptide 1..27
FT FT /note= "Signal peptide"
FT Protein 28..129
FT FT /note= "Mature human TWEAKR protein"
FT Domain 79..101
FT FT /note= "Transmembrane domain"
FT Domain 102..129
FT FT /note= "Intracellular domain"

XX WO200145730-A2.
XX 28-JUN-2001.
XX 19-DEC-2000; 2000WO-US034755.
XX 20-DEC-1999; 99US-0172878P.
XX 10-MAY-2000; 2000US-0203347P.

XX (IMMV) IMMUNEX CORP.

XX Wilely SR;

WPI: 2001-417975/44.
N-PSDB; AAS03963.

Modulating angiogenesis in a mammal for treating diseases mediated by
angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or
peripheral tissue, by administering antagonist or agonist of TWEAK
receptor.

Example 1; Fig 1; 46pp; English.

The sequence represents the human TWEAK receptor (TWEAKR) protein. The
TWEAK protein is a member of the tumour necrosis factor (TNF) family and
induces angiogenesis. TWEAKR may therefore be used to screen for and
develop TWEAKR agonists and antagonists for the modulation of human
angiogenesis, to be used in the treatment and diagnosis of human disease.
The disorders mediated by angiogenesis include ocular disorders
characterised by ocular neovascularisation such as diabetic retinopathy,
neovascular glaucoma, retinoblastoma, retinopathy of prematurity,
retrolental fibroplasia, rubellosis, uveitis, macular degeneration and
corneal graft neovascularisation, and inflammatory diseases such as
arthritis, rheumatism and psoriasis. Other treatable diseases include
malignant and metastatic conditions such as sarcomas and carcinomas,
benign tumours and preneoplastic conditions, myocardial angiogenesis,
haemophilic joints, scleroderma, vascular adhesions, atherosclerotic
plaque neovascularisation, telangiectasia, wound granulation, coronary
atherosclerosis, peripheral atherosclerosis and ischaemia

Sequence 129 AA;

Query Match 93.9%; Score 571; DB 4; Length 129;
Best Local Similarity 94.7%; Pred. No. 8.4e-52;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
QY 61 SDFCLGCAAPAPPFRLLWPIILGALSILTFVLGLLGSFLVWRRRRSSPPPP 113
Db 61 SDFCLGCAAPAPPFRLLWPIILGALSILTFVLGLLGSFLVWRRRRREKFTTF 113

RESULT 5
ABP61512
ID ABP61512 standard; protein; 129 AA.

XX ABP61512;

XX 30-SEP-2002 (first entry)

XX Human NF-kB activating protein SEQ ID NO 178.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
XX immunomodulator; cycostatic; antiinfective; osteopathic; neutropic;
XX neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
XX bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP011389.

XX 28-DEC-2000; 2000JP-0040288.

XX 26-MAR-2001; 2001JP-00089912.

XX 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAH KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

DR WPI; 2002-583617/62.
 DR N-PSDB; ABQ92000.
 XX NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer.
 XX Claim 4; Page 814-815; 841pp; Japanese.
 XX The invention relates to a purified protein (1), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and
 CC for treating e.g. inflammations, autoimmune diseases, cancers,
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
 CC disorders
 XX Sequence 129 AA;
 SQ
 Query Match 93.9%; Score 571; DB 5; Length 129;
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 DB 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 QY 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRRCRRERSPPPP 113
 DB 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRRCRRREKFTTP 113
 RESULT 6
 AAU79827
 ID AAU79827 standard; protein; 129 AA.
 AC AAU79827;
 XX
 DT 15-JUL-2002 (first entry)
 DE Human type 1 transmembrane protein Fn14.
 XX Type 1 transmembrane protein Fn14; human; cytotostatic; cardiant;
 KW vulnery; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;
 KW tumour necrosis factor family; TNF family; TWEAK receptor;
 KW myocardial ischaemic condition; myocardial infarction; wound healing;
 KW burn healing; gastric ulcer; tissue transplantation; wound healing;
 KW organ transplantation; neovascularisation; vascular insufficiency;
 KW cancer; inflammatory macular degeneration; diabetic retinopathy.
 XX
 OS Homo sapiens.
 XX WO200222166-A2.
 PN 21-MAR-2002.
 XX 12-SEP-2001; 2001WO-US028451.
 XX 14-SEP-2000; 2000US-0232355P.
 XX (BIOJ) BIOGEN INC.
 XX Browning J, Burkly L, Jakubowski A, Zheng T;
 PI WPI; 2002-383103/41.
 XX Methods of modulating angiogenesis and inhibiting tumor progression,
 PT using TWEAK receptor agonists.
 XX Disclosure; Fig 10A; 37pp; English.
 PS

XX The invention describes methods of modulating angiogenesis and inhibiting
 CC tumour progression using TWEAK (a novel member of the tumour necrosis
 CC factor or TNF family) receptor agonists. Conditions which can be treated
 CC using the agonists include myocardial ischaemic conditions (e.g.
 CC myocardial infarction), wound healing (e.g. burn healing and healing of
 CC gastric ulcers), and tissue and organ transplantations to promote
 CC neovascularisation, particularly in subjects suffering from vascular
 CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and
 CC subsequently neovascularisation is useful in treatment of cancer,
 CC inflammatory macular degeneration and diabetic retinopathy. This sequence
 CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor
 CC described in the invention
 XX Sequence 129 AA;
 SQ
 Query Match 93.9%; Score 571; DB 5; Length 129;
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 DB 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
 QY 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRRCRRERSPPPP 113
 DB 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRRCRRREKFTTP 113
 RESULT 7
 ADA56889
 ID ADA56889 standard; protein; 129 AA.
 XX ADA56889;
 AC ADA56889;
 XX
 DT 20-NOV-2003 (first entry)
 DE Human secreted protein #172.
 XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
 KW cytotostatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.
 XX Homo sapiens.
 OS
 XX WO2002102994-A2.
 PN 27-DEC-2002.
 XX 19-MAR-2002; 2002WO-US008278.
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 PI WPI; 2003-167512/16.
 DR N-PSDB; ADA55993.
 XX New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 XX neurodegenerative disorders.
 XX

Claim 13; SEQ ID NO 1079; 175app; English.

The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that bind to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. Parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 129 AA;

Query Match 93.9%; Score 571; DB 6; Length 129;
Best Local Similarity 94.7%; Pred. No. 8.4e-52;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARHP 60
DB 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARHP 60
QY 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLSGFLVWRCRRERSPP 113
DB 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLSGFLVWRCRRERKFTTP 113

RESULT 8
ABU56716
ID ABU56716 standard; protein; 129 AA.
XX AC
XX ABU56716;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide #309.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX W0200286443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012476.

XX 18-APR-2001; 2001US-0284770P.

PR 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
PI WPI; 2003-093161/08.
XX N-PSDB; ABX76445.

DR Detecting a lung cancer-associated transcript in a cell from a patient
DR for treating lung cancer, by contacting a biological sample from the
DR patient with a polynucleotide that exhibits increased or decreased
DR expression in lung cancer.

Claim 27; Page 429; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
XX invention

Sequence 129 AA;

Query Match 93.9%; Score 571; DB 6; Length 129;
Best Local Similarity 94.7%; Pred. No. 8.4e-52;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARHP 60
DB 1 MARGSLRLRLLLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARHP 60
QY 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLSGFLVWRCRRERSPP 113
DB 61 SDFCLGCAAAPAPFRLWLPILGGALSLTFVLGSLSGFLVWRCRRERKFTTP 113

RESULT 9
ADC74112

ID ADC74112 standard; protein; 129 AA.

XX AC ADC74112;

XX 01-JAN-2004 (first entry)

XX Human secreted protein - SEQ ID 745.

XX antianemic; anti-rheumatic; antiarthritic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotropic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;

KW human.
 XX Homo sapiens.
 OS WO20003038063-A2.
 XX PD 08-MAY-2003.
 XX PF 19-MAR-2002; 2002WO-US008277.
 XX PR 21-MAR-2001; 2001US-0277340P.
 XX PR 19-JUL-2001; 2001US-0306171P.
 XX PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX WPI; 2003-430516/40.
 XX DR N-PSDB; ADC73497.
 XX PT New human secreted polypeptide for diagnosing, preventing or treating
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 PT atherosclerosis).
 XX Claim 16; SEQ ID NO 745; 2272pp; English.
 XX The invention relates to a novel human secreted polypeptide comprising a
 CC defined sequence given in the specification. The polypeptide, nucleic
 CC acid molecule, antibody, agonist or antagonist of the invention may be
 CC useful for preparing a composition for diagnosing or treating a
 CC haemopoietic or haematologic disorder such as anaemia, autoimmune
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
 CC parasitic infections. The polypeptide may also be used during gene
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein of the
 CC invention.
 XX Sequence 129 AA;
 SQ
 Query Match 93.9%; Score 571; DB 7; Length 129;
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MARGSLRLRLVLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60
 DB 1 MARGSLRLRLVLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60
 QY 61 SDFCLGCAAPAPFRLWLLPILGALSITFVLGLSGFLVWRRCRRSSPPP 113
 DB 61 SDFCLGCAAPAPFRLWLLPILGALSITFVLGLSGFLVWRRCRRREKFTTP 113
 RESULT 10
 ADD37867
 ID ADD37867 standard; protein; 129 AA.
 XX ADD37867;
 AC
 XX 15-JAN-2004 (first entry)
 DT
 XX Human secreted protein #50.
 DE
 XX human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
 KW

OS Homo sapiens.
 XX WO200290526-A2.
 XX PD 14-NOV-2002.
 XX PF 19-MAR-2002; 2002WO-US008279.
 XX PR 21-MAR-2001; 2001US-0277340P.
 XX PR 19-JUL-2001; 2001US-0306171P.
 XX PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX WPI; 2003-140218/13.
 XX DR
 XX PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing or
 PT treating allergic or asthmatic disorders, or related immediate
 PT hypersensitivity disorders.
 XX Claim 1; SEQ ID NO 349; 1323pp; English.
 XX The present invention relates to an isolated polypeptide or human
 CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
 CC their fragments, and agonists or antagonists that bind are useful for
 CC preparing a diagnostic or pharmaceutical composition for diagnosing or
 CC treating allergic or asthmatic disorders. The polypeptide is also useful
 CC for identifying a binding partner by contacting the polypeptide with a
 CC binding partner, and determining whether the binding partner increases or
 CC decreases the activity of the polypeptide. The polypeptides and nucleic
 CC acid molecules are also useful for detecting, preventing, diagnosing,
 CC prognosticating, treating or ameliorating inflammatory disorders
 CC neoplastic diseases, wound healing and disorders of epithelial cell
 CC proliferation, immune disorders, cardiovascular disorders, blood-related
 CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
 CC disorders. The nucleic acids are also useful for chromosome
 CC identification, radiation hybrid mapping or long-range restriction
 CC mapping, as molecular weight markers, or as hybridization or diagnostic
 CC probes. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The present sequence represents a human
 CC secreted protein.
 XX Sequence 129 AA;
 SQ
 Query Match 93.9%; Score 571; DB 7; Length 129;
 Best Local Similarity 94.7%; Pred. No. 8.4e-52;
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MARGSLRLRLVLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60
 DB 1 MARGSLRLRLVLGLWLLRLSVAGEQAPGTAPCSRGSWSADLDKCMDASCARPH 60
 QY 61 SDFCLGCAAPAPFRLWLLPILGALSITFVLGLSGFLVWRRCRRSSPPP 113
 DB 61 SDFCLGCAAPAPFRLWLLPILGALSITFVLGLSGFLVWRRCRRREKFTTP 113
 RESULT 11
 ADD89033
 ID ADD89033 standard; protein; 129 AA.
 XX ADD89033;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX TAT274.
 DE
 XX tumour-associated antigenic target polypeptide; Cytostatic; tumour;
 KW cancer.
 KW


```
XX FH Key Location/Qualifiers
XX FT Peptide 1..27
XX FT Protein /note= "Signal peptide"
XX FT Protein 28..309
XX FT Protein /note= "Mature human TWEAKR-Fc fusion protein.
XX FT Protein Specifically referred to in Claim 11"
XX FT Domain 28..79
XX FT /note= "From TWEAKR extracellular domain. Specifically
XX FT referred to in Claims 4 and 10"
XX FT Region 80..81
XX FT /note= "From a BgIII cloning site"
XX FT Region 82..309
XX FT /note= "Fc portion"
XX FN WO200145730-A2.
XX PN
XX XX 28-JUN-2001.
XX PD
XX XX 19-DEC-2000; 2000WO-US034755.
XX PF
XX XX 20-DEC-1999; 99US-0172878P.
XX PR
XX XX 10-MAY-2000; 2000US-0203347P.
XX PF
XX PA (IMVU) IMMUNEX CORP.
XX XX
XX XX Wiley SR;
XX PI
XX XX WPT; 2001-417975/44.
XX DR
XX DR N-PSDB; AAS03965.
XX XX
XX XX Modulating angiogenesis in a mammal for treating diseases mediated by
XX PT angiogenesis; e.g. solid tumors and vascular deficiencies of cardiac or
XX PT peripheral tissue, by administering antagonist or agonist of TWEAK
XX PT receptor.
XX PS
XX PS Claim 4; Page 45-46; 46pp; English.
XX CC
XX CC The sequence represents a fusion protein consisting of the human TWEAK
XX CC receptor (TWEAKR) protein extracellular domain fused to an Fc portion
XX CC from human IgG1. This fusion protein, TWEAKR-Fc, is used in the
XX CC preparation of TWEAKR agonists and antagonists. The TWEAKR protein is a
XX CC member of the tumour necrosis factor (TNF) family and induces
XX CC angiogenesis. TWEAKR may therefore be used to screen for and develop
XX CC TWEAKR agonists and antagonists for the modulation of angiogenesis, to be
XX CC used in the treatment and diagnosis of human disease. The disorders
XX CC mediated by angiogenesis include ocular disorders characterised by ocular
XX CC neovascularisation such as diabetic retinopathy, neovascular glaucoma,
XX CC retinoblastoma, retinopathy of prematurity, retrolental fibroplasia,
XX CC rubeosis, uveitis, macular degeneration and corneal graft
XX CC neovascularisation, and inflammatory diseases such as arthritis,
XX CC rheumatism and psoriasis. Other treatable diseases include malignant and
XX CC metastatic conditions such as sarcomas and carcinomas, benign tumours and
XX CC preneoplastic conditions, myocardial angiogenesis, haemophilic joints,
XX CC scleroderma, vascular adhesions, atherosclerotic plaque
XX CC neovascularisation, telangiectasia, wound granulation, coronary
XX CC atherosclerosis, peripheral atherosclerosis and ischaemia
XX PS
XX PS Sequence 309 AA;
XX CC
XX CC Query Match 71.2%; Score 433; DB 4; Length 309;
XX CC Best Local Similarity 74.1%; Pred. No. 5.7e-37;
XX CC Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;
XX QY 1 MARGSLRLLRLVLLGLMALLRSVAGQAPGTCRSGSSWSADLDKCMCASCARPH 60
XX DB 1 MARGSLRLLRLVLLGLMALLRSVAGQAPGTCRSGSSWSADLDKCMCASCARPH 60
XX QY 61 SDFCLGCAAPAPPRLLWPIILGGALLSLTFVLGSLFVWRCCRERSPP 112
XX DB 61 SDFCLGCAAPAPPRLLWPIILGGALLSLTFVLGSLFVWRCCRERSPP 90
```

```
RESULT 14
AA91463
ID AA91463 standard; protein; 112 AA.
XX
XX AA91463;
XX
XX 29-JUN-2000 (first entry)
XX
XX Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.
XX
XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
XX antiHIV; antiinflammatory; neutropic; neuroprotective; antiallergic;
XX osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
XX antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
XX immune disease; inflammation; blood disorder; tumour; chromosome 16.
XX
XX Homo sapiens.
XX OS
XX XX WO200006698-A1.
XX PN
XX XX 10-FEB-2000.
XX PD
XX XX 29-JUL-1999; 99WO-US017130.
XX PF
XX XX 30-JUL-1998; 98US-0094657P.
XX PR
XX XX 05-AUG-1998; 98US-0095486P.
XX PR
XX XX 06-AUG-1998; 98US-0095454P.
XX PR
XX XX 06-AUG-1998; 98US-0095455P.
XX PR
XX XX 12-AUG-1998; 98US-0096319P.
XX PR
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX XX Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
XX PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
XX PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX XX
XX WPI; 2000-195282/17.
XX DR
XX DR N-PSDB; AAA26358.
XX XX
XX XX New isolated human genes and the secreted polypeptides they encode,
XX PT useful for diagnosis and treatment of e.g. cancers, neurological
XX FT disorders, immune diseases, inflammation or blood disorders.
XX XX
XX PS Claim 11; Page 465; 634pp; English.
XX CC
XX CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the
XX CC human secreted proteins given in AA91451 to AA91691. The human secreted
XX CC proteins can have activities based on the tissues and cells they are
XX CC expressed in. Examples of the activities are: cytostatic;
XX CC immunosuppressive; antiHIV; antiinflammatory; neutropic; neuroprotective;
XX CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
XX CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
XX CC corresponding secreted proteins are useful for preventing, treating or
XX CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
XX CC pathological conditions can be diagnosed by determining the amount of the
XX CC proteins in a sample or by determining the presence of mutations in the
XX CC polynucleotides. Specific uses are described for each of the
XX CC polynucleotides, based on which tissues they are most highly expressed
XX CC in, and include developing products for the diagnosis or treatment of
XX CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
XX CC and foetal deficiencies, blood disorders, diseases of the immune system,
XX CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
XX CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
XX CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
XX CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
XX CC reproductive disorders, gastrointestinal disorders, respiratory disorders
XX CC and metabolic disorders. The proteins or polynucleotides can also be used
XX CC as food additives or preservatives. The proteins are also useful for
XX CC identifying their binding partners. AAA26337 to AAA26345 and AA91450 are
XX CC sequences used in the exemplification of the present invention
XX PS
XX PS Sequence 112 AA;
```


Query Match 45.1%; Score 274.5; DB 3; Length 112;
 Best Local Similarity 96.4%; Pred. No. 7.2e-21;
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCA-SC 55
 DB 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCTSC 56

RESULT 15
 ADA57390
 ID ADA57390 standard; protein; 112 AA.
 AC ADA57390;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein #172.
 XX
 KW immunosuppressive; antiinflammatory; antilasthmatic; antiallergic;
 KW cytotstatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.
 XX
 OS Homo sapiens.
 XX
 PN WO2002102994-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002WO-US008278.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Rosen CA, Ruben SM;
 PI
 XX WPI; 2003-167512/16.
 DR N-PSDB; ADA56496.
 XX
 PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 XX
 PS Claim 13; SEQ ID NO 1582; 1754pp; English.

The invention relates to 592 new human secreted polypeptides useful for
 diagnosing, treating or preventing e.g. immune disorders, inflammatory
 conditions, respiratory disorders, cancers, CNS disorders, or
 neurodegenerative disorders, or polypeptides comprising an amino acid
 sequence at least 95% identical to the new sequences. The polypeptides,
 antibodies or antibody fragments that bind to the polypeptides, nucleic
 acids encoding the polypeptides, agonists or antagonists that binds to
 the polypeptide, are useful in preparing diagnostic or pharmaceutical
 compositions for diagnosing, treating or preventing an e.g. immune
 disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 polynucleotides are useful for chromosome identification, chromosome
 mapping, for controlling gene expression through triple helix formation
 or antisense DNA or RNA, in gene therapy, for identifying individuals

CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: The sequence data for
 CC this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 112 AA;

Query Match 45.1%; Score 274.5; DB 6; Length 112;
 Best Local Similarity 96.4%; Pred. No. 7.2e-21;
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCA-SC 55
 DB 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCTSC 56

Search completed: March 1, 2004, 16:42:52
 Job time : 77 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:41:53 ; Search time 23 Seconds
(without alignments)
255.885 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRLRLVGLVGLWLA.....LSGFLVWRCHRRSSPPXP 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	99.8	114	4	US-09-690-454-59
2	274.5	45.1	112	4	US-09-489-847-139
3	274.5	45.1	155	4	US-09-489-847-284
4	274.5	45.1	156	4	US-09-489-847-228
5	96.5	15.9	248	4	US-09-252-991A-29249
6	88.5	14.6	400	4	US-09-252-991A-26145
7	87.5	14.4	631	4	US-09-252-991A-20063
8	83.5	13.7	152	4	US-09-252-991A-31619
9	80.5	13.2	249	4	US-09-252-991A-23850
10	76.5	12.6	250	4	US-09-322-409-31
11	76.5	12.6	250	4	US-09-451-527-31
12	76.5	12.6	276	4	US-09-322-409-26
13	76.5	12.6	276	4	US-09-451-527-26
14	75	12.3	334	4	US-09-252-991A-18795
15	74.5	12.3	305	4	US-09-252-991A-21147
16	73.5	12.1	187	4	US-09-199-637A-287
17	73.5	12.1	187	4	US-09-252-991A-21454
18	72	11.8	1278	4	US-09-462-136-2
19	72	11.8	3724	2	US-08-804-227C-10
20	72	11.8	3724	2	US-08-804-198-4
21	71.5	11.8	478	4	US-09-252-991A-22078
22	70.5	11.6	402	4	US-09-252-991A-18195
23	69.5	11.4	176	4	US-09-252-991A-23290
24	69	11.3	152	4	US-09-252-991A-24730
25	69	11.3	153	4	US-09-252-991A-20688
26	69	11.3	215	3	US-09-220-528-104
27	69	11.3	511	4	US-09-252-991A-28223

28	68.5	11.3	127	4	US-09-489-039A-10884	Sequence 10884, A
29	68.5	11.3	205	2	US-08-775-009-37	Sequence 37, Appl
30	68.5	11.3	429	1	US-07-964-589-2	Sequence 2, Appli
31	68.5	11.3	429	5	PCT-US93-02024-2	Sequence 2, Appli
32	68	11.2	139	4	US-09-252-991A-17414	Sequence 17414, A
33	68	11.2	144	4	US-09-252-991A-17313	Sequence 17313, A
34	68	11.2	204	4	US-09-252-991A-29996	Sequence 29996, A
35	68	11.2	282	4	US-09-252-991A-29124	Sequence 29124, A
36	68	11.2	365	4	US-09-252-991A-31958	Sequence 31958, A
37	68	11.2	775	4	US-09-252-991A-22300	Sequence 22300, A
38	67.5	11.1	174	3	US-09-383-586-12	Sequence 12, Appl
39	67.5	11.1	268	4	US-09-322-409-23	Sequence 23, Appl
40	67.5	11.1	268	4	US-09-451-527-23	Sequence 23, Appl
41	67.5	11.1	294	4	US-09-322-409-7	Sequence 7, Appli
42	67.5	11.1	294	4	US-09-451-527-7	Sequence 7, Appli
43	67.5	11.1	359	3	US-09-413-814-90	Sequence 90, Appl
44	67.5	11.1	361	3	US-09-413-814-77	Sequence 77, Appl
45	67	11.0	112	4	US-09-252-991A-21707	Sequence 21707, A

ALIGNMENTS

RESULT 1

US-09-690-454-59
; Sequence 59, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-09-690-454-59

Query Match 99.8%; Score 607; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.5e-59;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRLRLVGLVGLWLA.....LSGFLVWRCHRRSSPPXP 60
DB 1 MARGSLRLRLVGLVGLWLA.....LSGFLVWRCHRRSSPPXP 60

Qy 61 SDFCLGCAAPAPPELLWPIILGGALSLTVLGLLGLVWRCRRSSPPP 113
Db 61 SDFCLGCAAPAPPELLWPIILGGALSLTVLGLLGLVWRCRRSSPPP 113

RESULT 2

US-09-489-847-139
; Sequence 139, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-139

Query Match 45.1%; Score 274.5; DB 4; Length 112;
Best Local Similarity 96.4%; Pred. No. 8.9e-23;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 3

US-09-489-847-284
; Sequence 284, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-284

Query Match 45.1%; Score 274.5; DB 4; Length 155;
Best Local Similarity 96.4%; Pred. No. 1.3e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 4

US-09-489-847-228
; Sequence 228, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 228
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-228

Query Match 45.1%; Score 274.5; DB 4; Length 156;
Best Local Similarity 96.4%; Pred. No. 1.3e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 5

US-09-252-991A-29249
; Sequence 29249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29249
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29249

Query Match 15.9%; Score 96.5; DB 4; Length 248;
Best Local Similarity 30.0%; Pred. No. 0.007;
Matches 27; Conservative 9; Mismatches 23; Indels 31; Gaps 4;

QY 18 WLALLRSVAGE-----QAGTAPCSRGS-----SWSADLDKCM 50
DB 38 WCSSTRSGGAACRCCRCASTAPCSRSASATAPRTGSCNCWAGAPTCWSATTSRCR 97
QY 51 DCASCRARPHSD--FCILGCA---AAPPAPR 76
DB 98 GCASSRRRTGTGWCACGAPVASPPAAWK 127

RESULT 6

US-09-252-991A-26145
; Sequence 26145, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26145
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26145

Query Match 14.6%; Score 88.5; DB 4; Length 400;
Best Local Similarity 38.3%; Pred. No. 0.091;
Matches 23; Conservative 4; Mismatches 30; Indels 3; Gaps 2;

QY 18 WLALLRSVAGEQAPGTAPCS--RGSSWSADLDKCMDCASCRRPHSDFCILGCA-AAPPAP 74
DB 45 WSTAWFPAPTAAGWPCRAWPMASNTATLSPTASCRPMHRCSCACCAKSRPPAP 104

RESULT 7

US-09-252-991A-20063
; Sequence 20063, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20063
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20063

Query Match 14.4%; Score 87.5; DB 4; Length 631;
Best Local Similarity 32.6%; Pred. No. 0.2;
Matches 30; Conservative 6; Mismatches 43; Indels 13; Gaps 4;

QY 23 RSVAGEQAPGTAPCSRGS--SWS-ADLDKCM--DCASCRARPHSDFCILGCAAPPAPRLL 78

DB 112 RSRKSRVPPAWPCVRGSRDWCAPMRACCRSCATCSATP-----AATPSAAACC 162
QY 79 WPILGALSLSLTVGLGSLGFLVWRRCRRRSS 110
DB 163 WCRAGVAARYAMKCGTLGASPTSCRRSSS 194

RESULT 8

US-09-252-991A-31619
; Sequence 31619, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31619
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31619

Query Match 13.7%; Score 83.5; DB 4; Length 152;
Best Local Similarity 29.7%; Pred. No. 0.11;
Matches 30; Conservative 7; Mismatches 37; Indels 27; Gaps 5;

QY 23 RSVAGEQAPGTAPCSRGSWSADLDKCMDC-----ASC--RAPHSDFCILGCAAPPAP 74
DB 63 RTTSNASRPTPARCSRHAPGWLGRACCGAAACGASCASATARPPT-----TAAWPPSS 117
QY 75 FRLLWPIIGALSILFVLGSLGFLVWRRCRR--RSPP 112
DB 118 APATWSASGGRCAGN-----WRECRAWGWRQSP 147

RESULT 9

US-09-252-991A-29850
; Sequence 29850, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29850
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29850

Query Match 13.2%; Score 80.5; DB 4; Length 249;
Best Local Similarity 30.5%; Pred. No. 0.4;
Matches 40; Conservative 8; Mismatches 32; Indels 51; Gaps 8;

QY 10 LRLLVLGLWMLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC-----RA 57
DB 104 LRVLRAAFCLLRVAVAGARLVAAAP--RGAGLAAPQS--PAASCANTSRTFTAPLRI 159

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; ORGANISM: Canis familiaris
US-09-451-527-31

Query Match      12.6%; Score 76.5; DB 4; Length 250;
Best Local Similarity 27.5%; Pred. No. 1.1;
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5

QY 11 RLIVLGIWLLALRSVAG-----EQAPCTAPCSRGSWSA 44
Db 49 RLVLAQRWVRLQAVGSQWILLAEVNTHEHVFVFCAFQDTSQOLAALKPWITRNFSG 108
QY 45 DLD-KCMDCASCRAHPHSDFCLGCAA--APPAPRLLWPILGGALSLTFVLGLLSGFLVW 101
Db 109 CLELQCPDSSTLVPPRSPGALATAPAPQAP-RLILLLL--LPVALLMSTAWCLHW 164
QY 102 RRCRRERSPP 112
Db 165 RRRRRRSPP 175

RESULT 12
US-09-322-409-26
; Sequence 26, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322.409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-26

Query Match      12.6%; Score 76.5; DB 4; Length 276;
Best Local Similarity 27.5%; Pred. No. 1.2;
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5

QY 11 RLIVLGIWLLALRSVAG-----EQAPCTAPCSRGSWSA 44
Db 75 RLVLAQRWVRLQAVGSQWILLAEVNTHEHVFVFCAFQDTSQOLAALKPWITRNFSG 134
QY 45 DLD-KCMDCASCRAHPHSDFCLGCAA--APPAPRLLWPILGGALSLTFVLGLLSGFLVW 101
Db 135 CLELQCPDSSTLVPPRSPGALATAPAPQAP-RLILLLL--LPVALLMSTAWCLHW 190
QY 102 RRCRRERSPP 112
Db 191 RRRRRRSPP 201

RESULT 13
US-09-451-527-26
; Sequence 26, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2

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; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-451-527-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;
Best Local Similarity 27.5%; Pred. No. 1.2;
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;
QY 11 RLVLGLWLLALLRSVAG-----EQAPGTAPCSRGSWSA 44
Db 75 RVLVAGRWVRLQAVAGSQMQLLEAVNTEIHVTFCAQDTSQQLAALKPWITRFSG 134
QY 45 DLD-KMDCASCARPHSDFCLGCAA--APPAPFLLWPIILGALSFLTFLVGLLSGLFLVW 101
Db 135 CLELQCPDSSTLVPSPGALATAPAPQAP-RLULLLL---LPVALLMSTANCLHW 190
QY 102 RRCRRERSPP 112
Db 191 RRRRRRSPP 201

RESULT 14
US-09-252-991A-18795
; Sequence 18795, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18795
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18795

Query Match 12.3%; Score 75; DB 4; Length 334;
Best Local Similarity 35.6%; Pred. No. 2.2;
Matches 26; Conservative 7; Mismatches 30; Indels 10; Gaps 4;
QY 33 TAPCSRGSSWSADLDKCMDCASCARPHSDFCLGCAAPAPPR--LLWPIILGALSFLT 90
Db 38 TPTTSTARSVRP-----APCLQAPAS--LLSTSTAPTATWADFLNALLAG-LALAL 89
QY 91 VLGLLSGFLVWRR 103
Db 90 VAGPLGSFVWRR 102

RESULT 15
US-09-252-991A-21147
; Sequence 21147, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21147
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21147

Query Match 12.3%; Score 74.5; DB 4; Length 305;
Best Local Similarity 29.1%; Pred. No. 2.3;
Matches 37; Conservative 10; Mismatches 61; Indels 19; Gaps 4;
QY 3 RGSRLRLRLLLVLGLWL---ALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRR 58
Db 20 RSTTRKPKAMCSLTWLABSTAAVPSWACSESPETLVMLRSWATWLCSSAAVAICWLR 79
QY 59 PHSDFCLGCA-----AAPAPFRLIW-----PILGALSFLT-----FVLGLLSGFLVWRR 103
Db 80 PSSSSTVATMRPSAWAALSASTFLLWMLALPRMAATASLAPSCNCSINPWISWVDCWVR 139
QY 104 CRRERS 110
Db 140 LASERTS 146

Search completed: March 1, 2004, 16:45:09
Job time : 24 secs


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;
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match
Best Local Similarity 99.8%; Score 607; DB 14; Length 114;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPP 113
Db 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPP 113

RESULT 2
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match
Best Local Similarity 99.8%; Score 607; DB 14; Length 114;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPP 113
Db 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPP 113
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Db 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPP 113

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match
Best Local Similarity 93.9%; Score 571; DB 9; Length 129;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPP 113
Db 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRREREKFTTP 113

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match
Best Local Similarity 93.9%; Score 571; DB 9; Length 129;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAAPAPPFRLWLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPP 113
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Db 61 SDFCLGCAAPPAPFRLLWPILGGALSFTFVLGLLSGFLVWRRCRREKETTP 113

RESULT 5

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RESULT 5
US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402088/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-178

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```
Query Match      93.9%; Score 571; DB 14; Length 129;
Best Local Similarity 94.7%; Pred. No. 6.3e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 1 MARGSLRRLRLVLGLWLLRLSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRAAPH 60

1 MARGSI RR LRL R L VI GI WL ALI RSVAGEO A PCT APCB GSSWSADI DKCWD CASCBAPPH 60

QY 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGILSGFLVRRRCRRERSPPP 113

61 SDECI GCAADPAPERLI WP7I GCNLSI TEVI CII SCETIMPPCBBEVEKTPD 113

POST-T 6

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RESULT 6
US-10-042-211A-178
; Sequence 178, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE OF INVENTION: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24

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; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-178

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Query Match 93.9%; Score 571; DB 14; Length 129;
Best Local Similarity 94.7%; Pred. No. 6.3e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVLGLWLLRSVAGEQPGTAPCSRGSSWSADLDKCMDASCRAAPH 60

db 1 MARGSLRRLLVLGLWLALLRSVAGEOAPGTAPCSRGSWSADLDKCMDCASCRAPH 60

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61 SDFCTGCCAAPPAPFRILMPILGGALSLTFTVLGIISGFIYVRRCTBRREKFTTP 113

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RESULT 7
US-10-331-496A-37
; Sequence 37, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,456A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,985
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 37
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-37

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Best Local Similarity 94.7%; Pred. No. 6.3e-48;
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1 MARGSLRLLRLVLGLWLALLRSVAGEOAPGTA PCSRGSSWSADLDKCMDCASCRAPH 60

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RESULT 8
US-10-295-027-444
; Sequence 444, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444

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; Sequence 1305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
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; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
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; PRIOR FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 2001-12-14
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; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
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US-10-295-027-1305

Query Match 93.9%; Score 571; DB 15; Length 129;
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Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGILSGFLVWRRCRERSPPPP 113
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RESULT 10
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; Sequence 5, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
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; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9
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Best Local Similarity 88.0%; Pred. No. 5.6e-29;
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; Sequence 4, Application US/10251947
; Publication No: US2003009990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-4
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Best Local Similarity 31.8%; Pred. No. 0.071;
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Job time : 47 secs

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(without alignments)
614.752 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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RESULT 1
PCT-US98-10868-60
Sequence 60, Application PC/TUS9810868
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: 32 Human Secreted Proteins
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/10868
FILING DATE: May 27, 1998
CLASSIFICATION:

ALIGNMENTS

1	607	99.8	114	1	PCT-US98-10868-60	Sequence 60, Appl
2	607	99.8	114	15	US-09-189-144-59	Sequence 59, Appl
3	607	99.8	114	26	US-10-062-593-59	Sequence 59, Appl
4	607	99.8	114	26	US-10-062-831-59	Sequence 59, Appl
5	571	93.9	129	1	PCT-US02-08277-745	Sequence 745, App
6	571	93.9	129	1	PCT-US02-08278-1079	Sequence 1079, App
7	571	93.9	129	1	PCT-US02-08279-349	Sequence 349, App
8	571	93.9	129	1	PCT-US02-41798A-37	Sequence 37, Appl
9	571	93.9	129	17	US-09-307-140-627	Sequence 627, App
10	571	93.9	129	17	US-09-316-633-265	Sequence 265, App
11	571	93.9	129	18	US-09-445-258-16	Sequence 16, Appl
12	571	93.9	129	18	US-09-445-258A-16	Sequence 16, Appl
13	571	93.9	129	18	US-09-465-587-220	Sequence 220, App
14	571	93.9	129	21	US-09-700-590A-64	Sequence 64, Appl
15	571	93.9	129	21	US-09-742-454A-4	Sequence 4, Appl
16	571	93.9	129	23	US-09-817-076-627	Sequence 627, App
17	571	93.9	129	23	US-09-883-777-4	Sequence 4, Appl
18	571	93.9	129	24	US-09-949-016-6914	Sequence 6914, App
19	571	93.9	129	26	US-10-024-298A-178	Sequence 178, App
20	571	93.9	129	26	US-10-042-211A-178	Sequence 178, App
21	571	93.9	129	27	US-10-126-052A-631	Sequence 631, App
22	571	93.9	129	28	US-10-295-027-444	Sequence 444, App
23	571	93.9	129	28	US-10-295-027-1305	Sequence 1305, App
24	571	93.9	129	29	US-10-331-496A-37	Sequence 37, Appl
25	571	93.9	129	30	US-10-405-027-4882	Sequence 4882, App
26	571	93.9	129	31	US-10-617-217A-178	Sequence 178, App
27	571	93.9	129	31	US-10-626-686-16	Sequence 16, Appl
28	571	93.9	129	33	US-60-109-869-2	Sequence 2, Appl
29	450	74.0	129	21	US-09-742-454A-5	Sequence 5, Appl
30	450	74.0	129	23	US-09-883-777-5	Sequence 7, Appl
31	433	71.2	309	21	US-09-742-454A-7	Sequence 7, Appl
32	433	71.2	309	23	US-09-883-777-7	Sequence 7, Appl
33	379.5	62.4	300	23	US-09-883-777-9	Sequence 9, Appl
34	336.5	55.3	94	30	US-10-405-027-4883	Sequence 4883, App
35	336.5	55.3	94	30	US-10-405-027-4884	Sequence 1095, App
36	274.5	45.1	112	1	PCT-US02-08277-1095	Sequence 1582, App
37	274.5	45.1	112	1	PCT-US02-08278-1592	Sequence 507, App
38	274.5	45.1	112	1	PCT-US02-08279-507	Sequence 136, App
39	274.5	45.1	112	1	PCT-US99-17130-136	Sequence 139, App
40	274.5	45.1	112	29	US-10-351-334-139	Sequence 3456, App
41	274.5	45.1	112	30	US-10-405-027-3456	Sequence 1096, App
42	274.5	45.1	155	1	PCT-US02-08277-1096	Sequence 1583, App
43	274.5	45.1	155	1	PCT-US02-08278-1593	Sequence 508, App
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45	274.5	45.1	155	1	PCT-US99-17130-277	

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PZ006PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US98-10868-60

Query Match 99.8%; Score 607; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.9e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-062-599-59
; Sequence 59, Application US/10062599
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match 99.8%; Score 607; DB 26; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.9e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-062-831-59
; Sequence 59, Application US/10062831
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
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FILE REFERENCE: P2006P1
CURRENT APPLICATION NUMBER: US/10/062.831
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: 09/690,454
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: PCT/US98/10868
PRIOR FILING DATE: May 28, 1998
PRIOR APPLICATION NUMBER: 60/044,039
PRIOR FILING DATE: May 30, 1997
PRIOR APPLICATION NUMBER: 60/048,093
PRIOR FILING DATE: May 30, 1997
PRIOR APPLICATION NUMBER: 60/048,190
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PRIOR FILING DATE: August 29, 1997
NUMBER OF SEQ ID NOS: 229
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: SITE
LOCATION: (114)
OTHER INFORMATION: Xaa equals stop translation

US-10-062-831-59

Query Match 99.8%; Score 607; DB 26; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.9e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAPAPPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERSPPPP 113
DB 61 SDFCLGCAAAPAPPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERSPPPP 113

RESULT 5
PCT-US02-08277-745
Sequence 745, Application PC/TUS0208277
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS907PCT
CURRENT APPLICATION NUMBER: PCT/US02/08277
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1357
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 745
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08277-745

Query Match 93.9%; Score 571; DB 1; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAPAPPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERSPPPP 113
DB 61 SDFCLGCAAAPAPPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERKFTTP 113

RESULT 6
PCT-US02-08278-1079
Sequence 1079, Application PC/TUS0208278
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS902PCT
CURRENT APPLICATION NUMBER: PCT/US02/08278
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1988
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1079
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08278-1079

Query Match 93.9%; Score 571; DB 1; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAPAPPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERSPPPP 113
DB 61 SDFCLGCAAAPAPPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRERKFTTP 113

RESULT 7
PCT-US02-08279-349
Sequence 349, Application PC/TUS0208279
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS903PCT
CURRENT APPLICATION NUMBER: PCT/US02/08279
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 642
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 349
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08279-349

Query Match 93.9%; Score 571; DB 1; Length 129;


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; Sequence 16, Application US/09445258
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
; APPLICANT: Kimura, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
; TITLE OF INVENTION: DOMAINS AND DNAs ENCODING THESE PROTEINS
; FILE REFERENCE: GIN-6706CFUS
; CURRENT APPLICATION NUMBER: US/09/445,258
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US98/02445
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: JP 9-144948
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-445-258-16

Query Match          93.9%; Score 571; DB 18; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCARPH 60
DB 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCARPH 60
QY 61 SDFCLGCAAAPAPFRLWLPILGGALSITFVLGLSGFLVWRCRRERSPP 113
DB 61 SDFCLGCAAAPAPFRLWLPILGGALSITFVLGLSGFLVWRCRRERKFTTP 113

RESULT 12
US-09-445-258A-16
; Sequence 16, Application US/09445258A
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
; APPLICANT: Kimura, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
; TITLE OF INVENTION: DOMAINS AND DNAs ENCODING THESE PROTEINS
; FILE REFERENCE: GIN-6706CFUS
; CURRENT APPLICATION NUMBER: US/09/445,258A
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US98/02445
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: JP 9-144948
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-445-258A-16

Query Match          93.9%; Score 571; DB 18; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCARPH 60
DB 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCARPH 60
QY 61 SDFCLGCAAAPAPFRLWLPILGGALSITFVLGLSGFLVWRCRRERSPP 113
DB 61 SDFCLGCAAAPAPFRLWLPILGGALSITFVLGLSGFLVWRCRRERKFTTP 113

RESULT 13
US-09-445-258A-16
; Sequence 16, Application US/09445258A
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
; APPLICANT: Kimura, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
; TITLE OF INVENTION: DOMAINS AND DNAs ENCODING THESE PROTEINS
; FILE REFERENCE: GIN-6706CFUS
; CURRENT APPLICATION NUMBER: US/09/445,258A
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US98/02445
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: JP 9-144948
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-445-258A-16

Query Match          93.9%; Score 571; DB 18; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCARPH 60
DB 1 MARGSLRRLRLVGLWLLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCARPH 60
QY 61 SDFCLGCAAAPAPFRLWLPILGGALSITFVLGLSGFLVWRCRRERSPP 113
DB 61 SDFCLGCAAAPAPFRLWLPILGGALSITFVLGLSGFLVWRCRRERKFTTP 113

RESULT 14
US-09-700-590A-64
; Sequence 64, Application US/09700590A
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YUE, Henry
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: BANDMAN, Olga
; APPLICANT: PATTERSON, Chandra
; APPLICANT: GORGONE, Gina A.
; APPLICANT: KASER, Matthew R.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: HUMAN TRANSMEMBRANE PROTEINS
; FILE REFERENCE: PF-0526 USN
; CURRENT APPLICATION NUMBER: US/09/700,590A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/087,260
; PRIOR FILING DATE: 05-29-1998
; PRIOR APPLICATION NUMBER: 60/091,674
; PRIOR FILING DATE: 07-02-1998
; PRIOR APPLICATION NUMBER: 60/102,954
; PRIOR FILING DATE: 10-02-1998
; PRIOR APPLICATION NUMBER: 60/109,869
; PRIOR FILING DATE: 11-24-1998
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PERL Program
; SEQ ID NO 64
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2454048
US-09-700-590A-64

Query Match      93.9%; Score 571; DB 21; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
   |||||||
Db 1 MARGSLRRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
   |||||||

Qy 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVGLLSGFLVWRCRRERSPPPP 113
   |||||||
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVGLLSGFLVWRCRREREKFTTP 113
   |||||||

RESULT 15
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      93.9%; Score 571; DB 21; Length 129;
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
   |||||||
Db 1 MARGSLRRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
   |||||||

Qy 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVGLLSGFLVWRCRRERSPPPP 113
   |||||||
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVGLLSGFLVWRCRREREKFTTP 113
   |||||||
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Search completed: March 1, 2004, 16:48:23
Job time : 182 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:43:08 ; Search time 10 Seconds
(without alignments)
102.79% Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRRLLLVGLWLA.....LSGFLVWRRCRRSSPPX 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 99762 seqs, 9017151 residues

Total number of hits satisfying chosen parameters: 99762

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/1/paa/PCT NEW COMB.ppt.*
- 2: /cgn2_6/ptodata/1/paa/US06 NEW COMB.ppt.*
- 3: /cgn2_6/ptodata/1/paa/US07 NEW COMB.ppt.*
- 4: /cgn2_6/ptodata/1/paa/US08 NEW COMB.ppt.*
- 5: /cgn2_6/ptodata/1/paa/US09 NEW COMB.ppt.*
- 6: /cgn2_6/ptodata/1/paa/US10 NEW COMB.ppt.*
- 7: /cgn2_6/ptodata/1/paa/US60 NEW COMB.ppt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	13.8	152	6	US-10-767-701-33810
2	71	11.7	123	6	US-10-773-236-290
3	67.5	11.1	368	6	US-10-667-762-10
4	66.5	10.9	229	6	US-10-767-701-46659
5	66	10.9	1238	6	US-10-762-603-4
6	65.5	10.8	271	6	US-10-417-375A-11
7	65	10.7	189	6	US-10-767-701-43640
8	64.5	10.6	1417	6	US-10-767-471-1010
9	64.5	10.6	1421	6	US-10-767-471-1009
10	64.5	10.6	1557	6	US-10-767-471-1011
11	64.5	10.6	1557	6	US-10-767-471-1014
12	64.5	10.6	1587	6	US-10-767-471-1013
13	64.5	10.6	1587	6	US-10-767-471-1015
14	64.5	10.6	1664	6	US-10-767-471-1012
15	64	10.5	115	6	US-10-333-177-2
16	63.5	10.4	126	6	US-10-767-701-60623
17	63.5	10.4	138	6	US-10-767-701-58471
18	63.5	10.4	150	6	US-10-767-701-54494
19	63.5	10.4	161	6	US-10-767-701-41647
20	63.5	10.4	193	6	US-10-767-701-33811
21	63.5	10.4	390	6	US-10-767-701-38237
22	63.5	10.4	476	1	PCT-US04-03417-8
23	63.5	10.4	476	6	US-10-772-636-8
24	62.5	10.3	283	6	US-10-451-467A-76
25	62.5	10.3	355	6	US-10-767-701-37723
26	62.5	10.3	854	6	US-10-767-471-910

27	62.5	10.3	1080	6	US-10-767-471-927	Sequence 927, App
28	62.5	10.3	1080	6	US-10-767-471-934	Sequence 934, App
29	62.5	10.3	1333	6	US-10-646-301A-12	Sequence 12, Appl
30	62.5	10.3	1333	6	US-10-663-208A-12	Sequence 12, Appl
31	62.5	10.3	2003	6	US-10-767-471-911	Sequence 911, App
32	62.5	10.3	2003	6	US-10-767-471-932	Sequence 932, App
33	62	10.2	108	6	US-10-767-701-50873	Sequence 50873, A
34	62	10.2	181	6	US-10-767-701-58367	Sequence 58367, A
35	61.5	10.1	216	6	US-10-767-701-38701	Sequence 38701, A
36	61	10.0	71	6	US-10-417-884A-4242	Sequence 4242, Ap
37	61	10.0	359	7	US-60-542-038-26	Sequence 26, Appl
38	60.5	10.0	168	6	US-10-767-701-35705	Sequence 35705, A
39	60.5	10.0	255	6	US-10-767-701-38374	Sequence 38374, A
40	60.5	10.0	1615	6	US-10-653-913-2	Sequence 2, Appl
41	60	9.9	113	6	US-10-767-701-31947	Sequence 31947, A
42	60	9.9	206	6	US-10-767-701-46607	Sequence 46607, A
43	60	9.9	228	6	US-10-767-701-42473	Sequence 42473, A
44	60	9.9	987	1	PCT-US04-02188-121	Sequence 121, App
45	60	9.9	987	6	US-10-764-425-121	Sequence 121, App

ALIGNMENTS

RESULT 1

US-10-767-701-33810
; Sequence 33810, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 33810
; LENGTH: 152
; TYPE: PNT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C37651_1.ppt
US-10-767-701-33810

Query Match		13.8%	Score 84;	DB 6;	Length 152;
Best Local Similarity		29.9%	Pred. No. 0.12;		
Matches		35;	Conservative	3;	Mismatches 25; Indels 54; Gaps 7;
QY	29	QAPGTAPCSR-----	-----GSSWSAD-LDKCMDASCARPHSDFC-----	64	
Db	23	QAPGLAPAPRRRLLLCGDPGAGCWTALAWCCRAPPCRLAP-----	-----CPTALPALPG	78	
QY	65	---LGCRAAPAPAPRLLMPILGGALSITFV-----	-----LGLLS---GFLVWRRCRR	106	
Db	79	AGSLASCAAPP-----	-----GSASMTVVRPATALLLGLSSAPGPWAPRCRR	124	

RESULT 2

US-10-773-236-290
; Sequence 290, Application US/10773236
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al.
; TITLE OF INVENTION: 89 Human Secreted Proteins
; FILE REFERENCE: PS751P1
; CURRENT APPLICATION NUMBER: US/10/773,236
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/311,085
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,209
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/US02/25107
; PRIOR FILING DATE: 2002-08-08

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; PRIOR APPLICATION NUMBER: 60/330,629
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US02/33985
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/331,046
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US02/35606
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/358,554
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US03/04819
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/358,714
; PRIOR FILING DATE: 2002-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 396
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 290
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-10-773-236-290

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Query Match 11.7%; Score 71; DB 6; Length 123;
Best Local Similarity 32.0%; Pred. No. 1.6;
Matches 24; Conservative 5; Mismatches 26; Indels 20; Gaps 5;

QY 31 PGTPAPCSRG--SSWSAD---LDKMDC--ASCRARPHSDFCLG-----CAAAP 71
Db 40 PGWSGSPSLGSCWCKTEGLLRCLQNAVATCRPTSDLLGLGRAVSSWORTLLCCPGP 99
QY 72 PAPFRLWPILGGAL 86
Db 100 SXASRVTPW-LAGAL 113

```

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RESULT 3
US-10-667-762-10
; Sequence 10, Application US/10667762
; GENERAL INFORMATION:
; APPLICANT: Erding Hu
; APPLICANT: Yuan Zhu
; APPLICANT: Ganesh M. Sathe
; APPLICANT: Joyce Yue Mao
; APPLICANT: Wendy S. Halsey
; APPLICANT: Jon Chambers
; APPLICANT: Alison Isobel Muir
; APPLICANT: Philip Graham Szekeres
; APPLICANT: Usman Shabon
; APPLICANT: Derk J. Bergema
; APPLICANT: Nabil A. Elshourbagy
; APPLICANT: David Michalovich
; APPLICANT: Pamela A. Lane
; APPLICANT: Menelas N. Pangalos
; APPLICANT: Melanie Robbins
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Jeffrey Hill
; APPLICANT: Ping Tsui
; APPLICANT: Pankaj Agarwal
; APPLICANT: Randall Forrest Smith
; APPLICANT: Lisa Vawter
; APPLICANT: Catherine E. Ellis
; APPLICANT: Manhanandeeshwar Gattu
; APPLICANT: John W. Quillen, Jr.
; APPLICANT: Erin M. Toland

Query Match 11.7%; Score 71; DB 6; Length 123;
Best Local Similarity 32.0%; Pred. No. 1.6;
Matches 24; Conservative 5; Mismatches 26; Indels 20; Gaps 5;

QY 31 PGTPAPCSRG--SSWSAD---LDKMDC--ASCRARPHSDFCLG-----CAAAP 71
Db 40 PGWSGSPSLGSCWCKTEGLLRCLQNAVATCRPTSDLLGLGRAVSSWORTLLCCPGP 99
QY 72 PAPFRLWPILGGAL 86
Db 100 SXASRVTPW-LAGAL 113

RESULT 4
US-10-767-701-46659
; Sequence 46659, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46659
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C104_76.pep
; US-10-767-701-46659

Query Match 10.9%; Score 66.5; DB 6; Length 229;
Best Local Similarity 28.7%; Pred. No. 7.7;
Matches 25; Conservative 8; Mismatches 29; Indels 25; Gaps 3;

QY 39 GSSWSADLD-KCMDACSC-----ARPHSDFCLCGAAPAPFRLWPIL----- 82
Db 104 GAAWSTTLKFKVNESYSCRYMLGSKNADITHSKLFNCTAEPSTTELLKLLILFSEMYV 163

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; APPLICANT: Steven Michael Poord
; APPLICANT: Han Ngoc Trinh
; APPLICANT: Alexander Taylor
; APPLICANT: Henry Sarau
; APPLICANT: Steven Ruben
; APPLICANT: George H. Poste
; APPLICANT: Michel Louis Souchet
; APPLICANT: Philippe Laurent Robert
; APPLICANT: Stephane Clement Krief
; APPLICANT: Bernard Emile Joseph Gout
; APPLICANT: Eve Mahe
; TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: GP-70775B-C1
; CURRENT APPLICATION NUMBER: US/10/667,762
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US/10/407,386
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/10/278,107
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/10/125,749
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US/09/988,922
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 368
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-10-667-762-10

Query Match 11.1%; Score 67.5; DB 6; Length 368;
Best Local Similarity 34.4%; Pred. No. 9.6;
Matches 21; Conservative 2; Mismatches 23; Indels 15; Gaps 2;

QY 65 LGCAAAP-----APFRLWPILGGALSLTFLVGLGSLFLVWRRRRSSP 111
Db 149 LGPPAPPAPARCSVLGGLGFPFLWALLAFALPALLLGAYGIFV--VARRAALRP 206
QY 112 P 112
Db 207 P 207

```



```
RESULT 9
US-10-767-471-1009
; Sequence 1009, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1009
; LENGTH: 1421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1009

Query Match      10.6%; Score 64.5; DB 6; Length 1421;
Best Local Similarity 29.7%; Pred. No. 85;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

Qy 36 CSRGSSWSADLDKCMDCASCARPHSDPCLGC-----AAAPPAPFRLWPILGGALSILT 89
Db 1174 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1218
;
Qy 90 FVLG 93
;
Db 1219 YEYG 1222
;

RESULT 10
US-10-767-471-1011
; Sequence 1011, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1011
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1011

Query Match      10.6%; Score 64.5; DB 6; Length 1557;
Best Local Similarity 29.7%; Pred. No. 70;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

Qy 36 CSRGSSWSADLDKCMDCASCARPHSDPCLGC-----AAAPPAPFRLWPILGGALSILT 89
Db 1310 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1354
;
Qy 90 FVLG 93
;
Db 1355 YEYG 1358
;

RESULT 11
US-10-767-471-1014
; Sequence 1014, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
```

```
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1014

Query Match      10.6%; Score 64.5; DB 6; Length 1557;
Best Local Similarity 29.7%; Pred. No. 70;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

Qy 36 CSRGSSWSADLDKCMDCASCARPHSDPCLGC-----AAAPPAPFRLWPILGGALSILT 89
Db 1310 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1354
;
Qy 90 FVLG 93
;
Db 1355 YEYG 1358
;

RESULT 12
US-10-767-471-1013
; Sequence 1013, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1013
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1013

Query Match      10.6%; Score 64.5; DB 6; Length 1587;
Best Local Similarity 29.7%; Pred. No. 72;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;

Qy 36 CSRGSSWSADLDKCMDCASCARPHSDPCLGC-----AAAPPAPFRLWPILGGALSILT 89
Db 1340 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1384
;
Qy 90 FVLG 93
;
Db 1385 YEYG 1388
;

RESULT 13
US-10-767-471-1015
; Sequence 1015, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-1015

Query Match      10.6%; Score 64.5; DB 6; Length 1587;
Best Local Similarity 29.7%; Pred. No. 72;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;
```

QY 36 CSRGSSWSADLDKMDCASCRARPHSDFCGLG-----AAAPAPERLLWPILGGALSIT 89
Db 1340 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1384
QY 90 FVLG 93
Db 1385 YEYG 1388

RESULT 14
US-10-767-471-1012
; Sequence 1012, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1012
; LENGTH: 1664
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1664)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-767-471-1012

Query Match 10.6%; Score 64.5; DB 6; Length 1664;
Best Local Similarity 29.7%; Pred. No. 75;
Matches 19; Conservative 4; Mismatches 20; Indels 21; Gaps 3;
QY 36 CSRGSSWSADLDKMDCASCRARPHSDFCGLG-----AAAPAPERLLWPILGGALSIT 89
Db 1335 CLYGEAWG-----MDCALCPAQSDDFEALCNVLRPPAYSPRP-----GGFGLP 1379

QY 90 FVLG 93
Db 1380 YEYG 1383

RESULT 15
US-10-333-177-2
; Sequence 2, Application US/10333177
; GENERAL INFORMATION:
; APPLICANT: Risssoan, Marie-Cloilde
; APPLICANT: Bridon, Jean-Michel
; APPLICANT: Duhen, Thomas
; APPLICANT: Briere, Francine
; APPLICANT: Bates, Elizabeth
; TITLE OF INVENTION: Type 2 Dendritic Cell Precursor Derived Coding Nucleic Acids and
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: SF01190
; CURRENT APPLICATION NUMBER: US/10/333,177
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: EP 00306087.8
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-333-177-2

Query Match 10.5%; Score 64; DB 6; Length 115;
Best Local Similarity 30.8%; Pred. No. 7;
Matches 16; Conservative 3; Mismatches 23; Indels 10; Gaps 2;

QY 29 QAP-----GTAPCSRGSSWSADLDKCM-DCASCRARPHSDFCGLGAAA 70
Db 4 QAPVVVVVTPQGVGPAPQNSNWOTGMCDFSDCGVCLGTCFPPCLGQVA 55

Search completed: March 1, 2004, 16:48:48
Job time : 13 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:59 ; Search time 21 Seconds
(without alignments)
522.183 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRLRLLLVLGLMLA.....LSGFLVWRRCRRRSPPXP 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78.5	12.9	332	2 T04484	probable chitinase
2	76.5	12.6	245	2 S78698	probable export pr
3	76.5	12.6	245	2 AD0753	flagellar biosynth
4	75.5	12.4	436	2 B70939	hypothetical prote
5	75.5	12.4	635	2 T20910	hypothetical prote
6	74.5	12.3	519	2 B87353	hypothetical prote
7	74	12.2	768	2 T22758	hypothetical prote
8	73.5	12.1	261	2 G69099	probable pyruvate
9	73	12.0	227	2 T04420	ribonuclease (EC 3
10	72.5	11.9	346	2 D75303	conserved hypothet
11	72	11.8	2871	2 A55624	fibrillin-1 precur
12	71	11.7	175	2 T36798	probable transcrip
13	70.5	11.6	467	2 E95850	probable amino aci
14	70	11.5	558	2 I56545	glypican precursor
15	69.5	11.4	424	2 D75330	probable beta-lact
16	69.5	11.4	587	2 C70893	hypothetical prote
17	69	11.3	324	2 JC2395	Fas antigen precur
18	68.5	11.3	431	1 B69092	conserved hypothet
19	68.5	11.3	484	2 E75138	osmoregulated prot
20	68	11.2	480	2 B61213	hypothetical prote
21	68	11.2	683	2 T00872	probable protein k
22	67.5	11.1	384	1 T46966	diheme cytochrome
23	67.5	11.1	1008	1 GNVUUK	glycoprotein precu
24	67.5	11.1	1013	2 I50615	receptor-type prot
25	67	11.0	319	2 JC4390	bone marrow stroma
26	67	11.0	332	2 A83572	oligopeptide trans
27	67	11.0	893	2 S51603	receptor-like tyro
28	67	11.0	898	2 S47489	receptor tyrosine
29	67	11.0	981	2 S51604	receptor-like tyro

ALIGNMENTS

RESULT 1

T04484

probable chitinase (EC 3.2.1.14) - barley

C:Species: Hordeum vulgare (barley)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: T04484

R:Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.

Plant J. 6, 579-589, 1994

A:Title: Identification of an enhancer/silencer sequence directing the aleurone-specific A:Reference number: Z15373; MUID:95078949; PMID:7987416

A:Accession: T04484

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-332 <LEA>

A:Cross-references: EMBL:L34211; NID:g576566; PIDN:AAA56787.1; PID:g507961

C:Genetics:

A:Gene: CH13

C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pla C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:28-69/Domain: hevein chitin-binding domain homology <HCB>

F:85-322/Domain: plant chitinase homology <PCH>

Query Match 12.9%; Score 78.5; DB 2; Length 332;
Best Local Similarity 32.0%; Pred. No. 3.5;
Matches 33; Conservative 9; Mismatches 38; Indels 23; Gaps 7;

QY 13 LVLGWLALLRSV---AGEQAPG-TAP-----CSRGSSWSADLDKMCDCASCRCARPHSDF 63

Db 13 IVLSAALAMVVRVRAQQCGSQAGGATCNCICCSRFVCGSTSDYC--GAGCQSQ----- 65

QY 64 CLGCAAPAPFRLWPIILGGALSLTFVLGLSGFLVWR-RCR 105

Db 66 CSGCGTPEGSP-----GGVSSIIISRDLEQQLHHRDRCQ 102

RESULT 2

S78698

probable export protein flip precursor - Salmonella typhimurium

C:Species: Salmonella typhimurium

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C:Accession: S78698

R:Ohnishi, K.; Fan, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.

J. Bacteriol. 179, 6092-6099, 1997

A:Title: The FlpO, FlpI, FlpQ, and FlpR proteins of Salmonella typhimurium: putative com A:Reference number: S78696; MUID:97464436; PMID:9324257

A:Accession: S78698

A:Molecule type: DNA

A:Residues: 1-245 <OHN>

A:Cross-references: EMBL:L49021; NID:gl066860; PIDN:AAB81319.1; PID:gl066863

A>Note: the sequence of residues 42-241 and the corresponding nucleic acid sequence are i

C:Genetics:

A:Gene: flp

A:Authors: Sqaers, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; PMID:98295987; PMID:9634230

[illegible]

```
A;Molecule type: DNA
A;Residues: 1-346 <WHI>
A;Cross-references: GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF11754.1; PID:g646000
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2205
A;Map position: 1

Query Match 11.9%; Score 72.5; DB 2; Length 346;
Best Local Similarity 28.8%; Pred. No. 13;
Matches 32; Conservative 10; Mismatches 52; Indels 17; Gaps 5;

QY 12 LLVLGLLALLRSVAGEQAPCTAPCSRGSWSADLDKCMDCASC---RAPHSD---FC 64
Db 87 LLVTCVGLGLV---TAGASPTV-----MWVGLVAAGAVLATVWHLRPAAGSLFFVFA 138

QY 65 LGCAAA--PPAPFELLPIGLGALSLLTFLVGLLGGFLVWRRCRRERSPPPP 113
Db 139 VGTVGALPHEPAPLPLALAVSGGAALSVALGALGAWHTRARPHELAAPPP 189

RESULT 11
A55624
fibrillin-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 24-Nov-2003
C;Accession: A55624
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez,
J. Biol. Chem. 270, 1798-1806, 1995
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ge
A;Reference number: A55624; MUID:95130561; PMID:7829516
A;Accession: A55624
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2871 <XIN>
A;Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
C;Genetics:
A;Gene: Fbn-1
C;Superfamily: fibrillin; EGF homology
F1201-1236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;
Best Local Similarity 25.3%; Pred. No. 75;
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

QY 36 CSRGSSWSADLDKMD-----CASCRARPHS-----DFCLGC 67
Db 2040 CPEGFSWSGRRQDLRMSYCYAKFEGKCSKSRNHSKQECCLAKGEGWGDPCCLC 2099

QY 68 AAAPPAPFRLIWPILGAL 86
Db 2100 PTEDEAFRQICPFGSGII 2118

RESULT 12
T36798
probable transcription regulator soxR-like - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T36798
R;Olivier, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21614
A;Accession: T36798
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-175 <OI>
A;Cross-references: EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEDB:SCI30A.18C
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCI30A.18C

Query Match 11.7%; Score 71; DB 2; Length 175;

A;Molecule type: DNA
A;Residues: 1-467 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC48469.1; PID:g15139941; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
Rebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMb20069
A;Genome: plasmid
C;Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 11.6%; Score 70.5; DB 2; Length 467;
Best Local Similarity 26.4%; Pred. No. 26;
Matches 28; Conservative 14; Mismatches 21; Indels 43; Gaps 7;

QY 10 LRLVLGLML-----ALLRSVAGEQA-PGTAPCSRGS-----SWGADLD 47
Db 322 LAIVSGVWASGETGAVLSAAFEALPG-----YGNLVITISLALFAFTTLGWAYAE 376

QY 48 KCMDCASCRPHSDFCLGCAAAPAPPAPFRLIWPFI---LGGALSITF 90
Db 377 KCW-----EYLIGTASA--IPFRIVTVAVFFGATSLDF 409

RESULT 14
I56545
Glypican precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 31-Jan-2000
C;Accession: I56545; JCI1281; FC1132
R;Litwack, E.D.; Stipp, C.S.; Kumbasar, A.; Lander, A.D.
J. Neurosci. 14, 3713-3724, 1994
A;Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-anc
A;Reference number: I56545; MUID:94267529; PMID:8207484
A;Accession: I56545
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-558 <RES>
A;Cross-references: GB:L34067; NID:g506416; PIDN:AAA41251.1; PID:g506417
R;Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.
Biochem. Biophys. Res. Commun. 188, 395-401, 1992
A;Title: Cloning of a major heparan sulfate proteoglycan from brain and identification as
```

A:Reference number: JCI281; MUID:93038690; PMID:1417860
A:Accession: JCI281
A:Molecule type: mRNA
A:Residues: 1-20,'T',22-311,'Y',313-361,'A',363-514,'I',516-558 <KAR>
A:Cross-references: GB:L02896; NID:G204424; PIDN:AAA6439.1; PID:G204425
A:Experimental source: brain
A:Accession: PC1132
A:Molecule type: protein
A:Residues: 24-55;424-445 <K2>
C:Superfamily: glypican
C:Keywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; heparan
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-530/Product: glypican #status predicted <MAT>
F:531-558/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:55,486,488,490/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F:79,116/Binding site: carboxylate (Asn) (covalent) #status predicted
F:399,512/Binding site: carboxylate (Thr) (covalent) #status predicted
F:530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match 11.5%; Score 70; DB 2; Length 558;
Best Local Similarity 37.7%; Pred. No. 33;
Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;

QY 11 RLVLGLWLA--LLRSVAGEQAPGTAPCSRGSSWSADLDKMDCASCR---ARPHSDFC 64
DB 221 RSFVQGLGVASDVVRKA--QVPLAECRA-----VMKLVYCAHCRGVGARPCPDYC 272

QY 65 ----LGCAG 69
DB 273 RNVKGCCLA 281

RESULT 15
D75330
probable beta-lactamase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: D75330
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75330
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-424 <WHI>
A:Cross-references: GB:AE002036; GB:AE000513; NID:G6459766; PIDN:AAF11537.1; PID:G645977
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRI985
A:Map position: 1

Query Match 11.4%; Score 69.5; DB 2; Length 424;
Best Local Similarity 29.7%; Pred. No. 30;
Matches 30; Conservative 11; Mismatches 35; Indels 25; Gaps 4;

QY 3 RGSRLRLRLVLGLMALRLRSVAGEQAPGTAPCSRGSSWSADLDKMDCASCR-----57
DB 2 RGTIRLTALLLG---AGINACRNEAQDTAPPAQAQAQAPRAKASASPAPTATE 58

QY 58 ----RPHSDFCLGCAA-----PPAPFLLWFLGALSL 88
DB 59 PAVSAPAAAGCLPAPAVTQAPRPQP-----LSGRGL 92

Search completed: March 1, 2004, 16:44:47
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:37:03 ; Search time 17 Seconds
(without alignments)
349,176 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRLRLRLVLGLWLA.....LSGFLVWRRCRRSSPPPX 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	571	93.9	129	1 FN14_HUMAN	Q9np84 homo sapien
2	445	73.2	129	1 FN14_MOUSE	Q9cr75 m tumor nec
3	87	14.3	184	1 T13C_HUMAN	Q96rj3 homo sapien
4	78	12.8	448	1 FBL5_RAT	Q9wvh8 rattus norv
5	77	12.7	448	1 FBL5_MOUSE	Q9wvh9 mus musculu
6	76.5	12.6	245	1 FLIP_SALTY	P54700 salmorella
7	74	12.2	548	1 LG13_MOUSE	Q8k406 mus musculu
8	73.5	12.1	81	1 PORD_METH	P56815 methanobact
9	72	11.8	1278	1 NPCL_HUMAN	O15118 homo sapien
10	72	11.8	2871	1 FBN1_MOUSE	Q61554 mus musculu
11	70	11.5	301	1 CTF5_HUMAN	Q9ujaz homo sapien
12	70	11.5	443	1 FBL4_MOUSE	Q9wvj9 mus musculu
13	70	11.5	558	1 GPC1_RAT	P35053 rattus norv
14	69.5	11.4	495	1 MLP2_DROME	Q24400 drosophila
15	69	11.3	180	1 PTTG_HUMAN	P53801 homo sapien
16	69	11.3	314	1 TR12_HUMAN	Q14140 homo sapien
17	69	11.3	324	1 TNR6_RAT	Q63199 rattus norv
18	68.5	11.3	205	1 GSGE_HUMAN	O15499 homo sapien
19	68.5	11.3	431	1 YG84_METH	Q27719 methanobact
20	67.5	11.1	368	1 GP62_HUMAN	P09zj7 homo sapien
21	67.5	11.1	1008	1 VGLM_YUK	P96133 ukuniemi v
22	67.5	11.1	1013	1 EPAS5_CHICK	P54755 gallus gall
23	67	11.0	279	1 CXE1_HUMAN	Q8afk1 homo sapien
24	67	11.0	319	1 BST1_RAT	Q63072 rattus norv
25	67	11.0	386	1 HXAD_MOUSE	Q62424 mus musculu
26	67	11.0	1005	1 EPAS5_RAT	P54757 rattus norv
27	67	11.0	2871	1 FBN1_PIG	Q9tcv36 sus scrofa
28	66.5	10.9	443	1 FBL4_CRIGR	O55058 cricetus
29	66	10.9	394	1 Y6B9_PSEAE	P42514 pseudomonas
30	66	10.9	992	1 POLS_RUBVM	P08563 rubella vir
31	66	10.9	1238	1 JAG2_HUMAN	Q9y219 homo sapien
32	66	10.9	2318	1 NTC3_MOUSE	Q61982 mus musculu
33	66	10.9	2319	1 NTC3_RAT	Q9r172 rattus norv

34	65.5	10.8	245	1 FLIP_ECOLI	P33133 escherichia
35	65.5	10.8	2321	1 NTC3_HUMAN	Q9um47 homo sapien
36	65	10.7	453	1 HRA3_HUMAN	P83110 homo sapien
37	65	10.7	1014	1 EPB6_MOUSE	O08644 mus musculu
38	65	10.7	1445	1 PTPG_HUMAN	P23470 homo sapien
39	64.5	10.6	112	1 PLAB_MOUSE	Q9ji48 mus musculu
40	64.5	10.6	123	1 VST1_HEVWE	O03499 hepatitis e
41	64.5	10.6	300	1 TRGB_HUMAN	O95407 homo sapien
42	64.5	10.6	443	1 FBL4_HUMAN	O95967 homo sapien
43	64	10.5	115	1 PLAB_HUMAN	Q9nzfl homo sapien
44	64	10.5	1210	1 EGFR_MOUSE	Q01279 mus musculu
45	64	10.5	1227	1 B3A3_MOUSE	P16283 mus musculu

ALIGNMENTS

RESULT 1
FN14_HUMAN STANDARD; PRT; 129 AA.
AC Q9NP84; Q9HC90;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member Fn14 precursor
DE (Fibroblast growth factor-inducible immediate-early response protein
DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).
GN TNFRSF12A OR FN14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=20216634; PubMed=10751351;
RA Feng S.-L.Y., Guo Y., Factor V.M., Thorgerirsson S.S., Bell D.W.,
RA Testa J.R., Peifley K.A., Winkles J.A.;
RT "The Fn14 immediate-early response gene is induced during liver
regeneration and highly expressed in both human and murine
hepatocellular carcinoma."
RT Am. J. Pathol. 156:1253-1261(2000).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Tanaka S., Sugimachi K.;
RT "Human homologue of Fn14."
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Uterus;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pailey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzyzanski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.

RESULT 2


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QY 108 RSSPPP 113
Db 121 KDAPEP 126

RESULT 4
FBL5 RAT STANDARD; PRT; 448 AA.
AC Q9WH8; Q9R284;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing
DE protein) (EVEC).
GN FBLN5 OR DANCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT "DANCE, a novel secreted RGD protein expressed in developing,
RT atherosclerotic, and balloon-injured arteries.";
RL J. Biol. Chem. 274:22476-22483 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99278197; PubMed=10347091;
RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;
RT "EVEC, a novel epidermal growth factor-like repeat-containing protein
RT upregulated in embryonic and diseased adult vasculature.";
RL Circ. Res. 84:1166-1176 (1999).
CC -!- FUNCTION: Promotes adhesion of endothelial cells through
CC interaction of integrins and the RGD motif. Could be a vascular
CC ligand for integrin receptors and may play a role in vascular
CC development and remodeling.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF112153; AAD41769.1; -
DR EMBL; AF137350; AAD25101.1; -
DR HSSP; P00736; IAPQ.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS50026; EGF_3; 5.
DR PROSITE; PS01187; EGF_CA; 6.
DR PROSITE; PS01187; EGF_CA; 6.
KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
KW Glycoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 448 FIBULIN-5.
FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT SITE 288 333 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT SITE 54 56 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 131 144 BY SIMILARITY.
FT DISULFID 138 153 BY SIMILARITY.
FT DISULFID 155 166 BY SIMILARITY.
FT DISULFID 172 181 BY SIMILARITY.
FT DISULFID 177 190 BY SIMILARITY.
FT DISULFID 192 205 BY SIMILARITY.
FT DISULFID 211 221 BY SIMILARITY.
FT DISULFID 217 230 BY SIMILARITY.
FT DISULFID 232 245 BY SIMILARITY.
FT DISULFID 251 262 BY SIMILARITY.
FT DISULFID 258 271 BY SIMILARITY.
FT DISULFID 273 286 BY SIMILARITY.
FT DISULFID 292 305 BY SIMILARITY.
FT DISULFID 320 332 BY SIMILARITY.
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 238 238 L -> P (IN REF. 2).
SQ SEQUENCE 448 AA; 50160 MW; E6BC68F7BF14B714 CRC64;

Query Match 12.8%; Score 78; DB 1; Length 448;
Best Local Similarity 24.1%; Pred. No. 2-2;
Matches 26; Conservative 8; Mismatches 24; Indels 50; Gaps 5;

QY 6 LRRLRLVLGLWLLRLRSVAGQAPGTA--PCSRGSSWSADLDKWCDCASCARPHSDF 63
Db 4 LKRILTVTLALWL-----PFGNAQQQTNGFDLDRGTGQCIDIDECRTIPEA-- 52

QY 64 CLG-----C-----AAAPPAP 74
Db 53 CRGDMCMVNGQGYLCIPRTNVPYRGPNPSTSYSGPYAAAPPVP 100

RESULT 5
FBL5_MOUSE STANDARD; PRT; 448 AA.
AC Q9WH9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibulin-5 precursor (FBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance).
GN FBLN5 OR DANCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT "DANCE, a novel secreted RGD protein expressed in developing,
RT atherosclerotic, and balloon-injured arteries.";
RL J. Biol. Chem. 274:22476-22483 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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KW Protein transport; Signal; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 245 FLAGELLAR BIOSYNTHETIC PROTEIN FLIP.
 FT TRANSMEM 45 65 POTENTIAL.
 FT TRANSMEM 88 108 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 209 229 POTENTIAL.
 SQ SEQUENCE 245 AA; C9A4241F0653A4D4 CRC64;
 Query Match 12.6%; Score 76.5; DB 1; Length 245;
 Best local similarity 30.8%; Pred. No. 1.8;
 Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;
 Y 6 LRRLLRLVLGLLALLRSVAGEAGP--TAP--CSRGSWSADLDKCMDCASCARP--- 59
 D 1 MRRLLFLSLAGLW--LSPRAAALPGLISQPLAGGQGSLSVQTUFTLSLTFLLPAIL 58
 Y 60 --HSDF-----CLGCAAAPPPAPFRLWPIILGGALSFTFVL 92
 D 59 LMTSFTRIIVFGLRLNLTGTPSAPNQV-----LLGLALFTFFI 100
 RESULT 7
 LG13 MOUSE
 ID LG13 MOUSE STANDARD; PRT; 548 AA.
 AC Q8K406;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Leucine-rich repeat LG1 family member 3 precursor (Leucine-rich
 DE glioma-inactivated protein 3) (Leubrin).
 GN LG13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saio R., Suzuki H., Yananaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Matals L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skolala U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- SIMILARITY: Contains 6 RAR repeats.
 CC -1- SIMILARITY: Contains 5 leucine-rich (LRR) repeats.
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 DR EMBL; AF515590; AAM55219.1; -
 DR EMBL; AV174077; AAO19739.1; -
 DR EMBL; AK049831; BAC33943.1; -
 DR EMBL; BC055315; AHH55315.1; -
 DR EMBL; BC061460; AAH61460.1; -
 DR MGD; MGI:2182619; Lgi3.
 DR InterPro; IPR009039; EAR.
 DR InterPro; IPR005492; EPTP.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR Pfam; PF03736; EPTP; 2.
 DR Pfam; PF00560; LRR; 3.
 DR Pfam; PF01463; LRRCT; 1.
 DR SMART; SM00369; LRR_TYP; 3.
 DR SMART; SM00082; LRRCT; 1.
 DR PROSITE; PSS0912; EAR; 6.
 DR Repeat; Leucine-rich repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 548
 FT REPEAT 63 86 LRR 1.
 FT REPEAT 87 110 LRR 2.
 FT REPEAT 112 134 LRR 3.
 FT REPEAT 135 158 LRR 4.
 FT REPEAT 160 183 LRR 5.
 FT REPEAT 221 264 EAR 1.
 FT REPEAT 267 310 EAR 2.
 FT REPEAT 313 361 EAR 3.
 FT REPEAT 362 406 EAR 4.
 FT REPEAT 409 453 EAR 5.
 FT REPEAT 454 497 EAR 6.
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 548 AA; 61817 MW; 2DB303936354B958 CRC64;
 Query Match 12.2%; Score 74; DB 1; Length 548;


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Db      235   TAPCS-----CQDCSIVGPKQ-----PppPPAP-----WTILGLDAMYVIM 273
QY      87   SUTFLVGLL----SGFLVWRRCRRR 108
           :|::|||:|::|||:|
Db      273   WITYMAFLLVFFGAFFAVM--CYRKX 296

RESULT 10
FBN1_MOUSE
ID FBN1_MOUSE STANDARD; PRT; 2871 AA.
AC Q61554; Q60826;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrillin-1 precursor.
GN FBN1 OR FBN-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
MD MEDLINE=95130561; PubMed=7829516;
RA Yin W., Germiller J., Sanguinetti C., Smiley E., Pangilinan T.,
RA Pereira L., Ramirez F., Bonadio J.;
RA "Primary structure and developmental expression of Fbn-1, the mouse
RL fibrillin gene.";
RL J. Biol. Chem. 270:1798-1806(1995).
RN [2]
RP SEQUENCE FROM N.A.
RS STRAIN=CD-1; TISSUE=Kidney;
RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Structural component of connective tissue microfibrils
CC that binds calcium. Fibrillin-1-containing support.
CC long-term force bearing structural support.
CC -!- PTM: Forms intermolecular disulfide bonds either with other
CC fibrillin-1 molecules or with other components of the microfibrils
CC (By similarity).
CC -!- SIMILARITY: Contains 47 EGF-like domains.
CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L29454; AAA56840.1; -
DR EMBL; U22493; AAA64217.1; -
DR PIR; A55624; A55624.
DR HSP; P35555; LAPJ.
DR MGD; MG1.95489; Fbnl.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 45.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00179; EGF_CA; 42.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS50026; EGF_3; 45.
DR PROSITE; PS01187; EGF_CA; 43.
KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
KW Repeat; Signal; Multigene family.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 2871 FIBRILLIN 1.
FT DOMAIN 81 112 EGF-LIKE 1.
FT DOMAIN 115 146 EGF-LIKE 2.
FT FT

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FT FT DISULFID 515 528 BY SIMILARITY.
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FT FT DISULFID 1617 1631 BY SIMILARITY.
FT FT DISULFID 1633 1646 BY SIMILARITY.
FT FT DISULFID 1652 1663 BY SIMILARITY.
FT FT DISULFID 1658 1672 BY SIMILARITY.

Query Match 11.8%; Score 72; DB 1; Length 2871;
Best Local Similarity 25.3%; Pred. No. 46;
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

Qy 36 CSRGSSWSADLDKQWD-----CASCRRAPHS-----DFCLGC 67
Db 2040 CPEGFSSSSRRRCQDLRMSYCYAKFEGKSSPKSRNHSKQECCKALKGEGWCDPCLC 2099
Qy 68 AAAPPAPFRLLWPILGAL 86

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Db 2100 PTEPDEAFRCICPGSGII 2118
RESULT 11
CTF5 HUMAN STANDARD; PRT; 301 AA.
ID OGUJ2:
AC 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein C20orf155.
GN C20ORF155.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver cancer;
RA Cheng Z., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McElay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Srapletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muszy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.C., Krzywinski M.I., Skaleka U., Smalls D.E.,
RA	Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-I- SUBUNIT: Binds preferentially to p53 mutants.
CC	-I- SUBCELLULAR LOCATION: Secreted.
CC	-I- SIMILARITY: Belongs to the fibulin family.
CC	-I- SIMILARITY: Contains 6 EGF-like domains.
CC	-----
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CC	between the Swiss Institute of Bioinformatics and the EMBL outpost at -
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CC	send an email to licens@isb-sib.ch).
CC	-----
DR	EMBL; AF104223; AAC45219.1; ;
DR	EMBL; BC012269; AAH12269.1; ;
DR	HSPG; P00736; IAPQ.
DR	MGD; MGI:1891209; Efemp2.
DR	InterPro; IPR000152; Asx_hydroxyyl_8.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR006209; EGF like.
DR	InterPro; IPR001491; Thrombosmodulin.
DR	Pfam; PF00008; EGF; 3.
DR	PRINTS; PR00907; THROMBOMODULIN.
DR	SMART; SM00179; EGF_CA; 4.
DR	PROSITE; PS00010; ASX_HYDROXYLYL; 4.
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.
DR	PROSITE; PS01186; EGF_2; 4.
DR	PROSITE; PS50026; EGF_3; 4.
DR	PROSITE; PS01187; EGF_CA; 6.
KW	Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
FT	SIGNAL 1 25 POTENTIAL.
FT	CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 2.
FT	FT DOMAIN 35 81 EGF-LIKE 1, DIVERGENT.
FT	FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	FT DOMAIN 243 282 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	FT DOMAIN 283 328 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	FT DISULFID 127 140 BY SIMILARITY.
FT	FT DISULFID 134 149 BY SIMILARITY.
FT	FT DISULFID 151 162 BY SIMILARITY.
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FT	FT DISULFID 287 300 BY SIMILARITY.
FT	FT DISULFID 294 309 BY SIMILARITY.
FT	FT DISULFID 315 327 BY SIMILARITY.

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 443 AA; 49425 MW; 4369C032A823DD88 CRC64;
 Query Match 11.5%; Score 70; DB 1; Length 443;
 Best Local Similarity 27.3%; Pred. No. 13;
 Matches 24; Conservative 5; Mismatches 33; Indels 26; Gaps 3;
 QY 13 LVGLWLAIRSVAGEAP---GTAPCSGSSWSADLCKMDCASCARPHS-----61
 Db 12 LLLWAFLLLLGAASPDPEEDSYTCTDGYEWDADSQHCRDYNELTTPCAKGBMKC 71
 QY 62 -----DFCLGCAAA-----PPAP 74
 Db 72 INHYGGVLCIPRSRAVLSLHGEGPPPP 99
 RESULT 13
 GPC1 RAT
 ID GPC1 RAT STANDARD; PRT; 558 AA.
 AC P35053;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Glypican-1 precursor (HSPG M12).
 GN GPC1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.
 RC TISSUE=Brain;
 RX MEDLINE=93038690; PubMed=1417860;
 RA Kartheikyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.;
 RT "Cloning of a major heparan sulfate proteoglycan from brain and
 RT identification as the rat form of glypican."
 RL Biochem. Biophys. Res. Commun. 188:395-401(1992).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.
 RC STRAIN=New England Deaconess Hospital;
 RX MEDLINE=94267529; PubMed=8207484;
 RA Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.;
 RT "Neuronal expression of glypican, a cell-surface
 RT glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan,
 RT in the adult rat nervous system."
 RL J. Neurosci. 14:3713-3724(1994).
 CC -!- FUNCTION: Cell surface proteoglycan that bears heparan sulfate.
 CC May play an important role in the trophic and injury responses of
 CC neurons.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Nervous system.
 CC -!- PTM: This cell-associated glypican is further processed to give
 CC rise to a medium-released species.
 CC -!- SIMILARITY: Belongs to the glypican family.
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 CC -----
 DR EMBL; L02896; AAA86439.1; -;
 DR EMBL; L34067; AAA41251.1; -;
 DR PIR; I56545; I56545.
 DR InterPro; IPR000024; Fz domain.
 DR Pfam; PF01153; Glypican.
 DR Pfam; PF01153; Glypican; 1.
 DR PROSITE; PS01207; GLYPICAN; 1.
 KW Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor;
 KW Extracellular matrix; Lipoprotein.

FT SIGNAL 1 23 GLYPICAN-1.
 FT CHAIN 24 530 REMOVED IN MATURE FORM (POTENTIAL).
 FT PROPEP 531 558 GPI-anchor amidated serine (POTENTIAL).
 FT LIPID 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 55 55 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT CARBOHYD 486 486 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT CARBOHYD 488 488 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT CARBOHYD 490 490 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT CARBOHYD 21 21 T -> A (IN REF. 2).
 FT CONFLICT 312 312 Y -> N (IN REF. 2).
 FT CONFLICT 362 362 A -> G (IN REF. 2).
 FT CONFLICT 437 437 I -> G (IN REF. 2; AA SEQUENCE).
 FT CONFLICT 443 443 E -> D (IN REF. 2; AA SEQUENCE).
 FT CONFLICT 515 515 I -> T (IN REF. 2).
 SQ SEQUENCE 558 AA; 61734 MW; E2878A854B9A1D7F CRC64;
 Query Match 11.5%; Score 70; DB 1; Length 558;
 Best Local Similarity 37.7%; Pred. No. 16;
 Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;
 QY 11 RLVLGLMLIA--LLRSVAGEAPGTAPCSGSSWSADLCKMDCASCRC-----ARPHSDFC 64
 Db 221 RSPVQGLGVASDVVRKVA--QVPLAPECGR-----VMKLVCACRGVPGARPCPDYC 272
 QY 65 -----LGCAG 69
 Db 273 RNVKLGCLA 281
 RESULT 14
 MLP2 DROME
 ID MLP2 DROME STANDARD; PRT; 495 AA.
 AC Q24400; Q9V162;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Muscle LIM protein MLP84B.
 GN LIM3 OR MLP84B OR CG10699.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96387325; PubMed=8794860;
 RA Stronach B.E., Siegrist S.E., Beckerle M.C.;
 RT "Two muscle-specific LIM proteins in Drosophila."
 RL J. Cell Biol. 134:1179-1195(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99326429; PubMed=10397768;
 RA Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.;
 RT "Muscle LIM proteins are associated with muscle sarcomeres and require
 RT dMEF2 for their expression during Drosophila myogenesis."
 RL Mol. Biol. Cell 10:2329-2342(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Neilson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclev J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2195(2000).
RL
CC -!- FUNCTION: Plays a role in cell differentiation late in myogenesis.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: In the embryo, expression is restricted to the
CC somatic, visceral, and pharyngeal muscles. Within the somatic
CC musculature, MLP498 is localized at the ends of muscles fibers at
CC the point of attachment to the epidermis. There is no expression
CC in cardiac mesoderm or in fat body.
CC -!- DEVELOPMENTAL STAGE: Expression is biphasic, peaking late in
CC embryogenesis (16-24 h embryos) and during the larval to pupal
CC transition, when the musculature is differentiating. Found in
CC developing muscles of the visceral and somatic mesoderm subsequent
CC to the formation of the muscle precursor cells. Decreased levels
CC are still detectable in adults.
CC -!- SIMILARITY: TO THE VERTEBRATE CYSTEINE-RICH PROTEINS.
CC -!- SIMILARITY: Contains 5 LIM zinc-binding domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X91245; CAA62627.1; -
DR EMBL; AF090832; AAC61591.1; -
DR EMBL; AE003672; AAF54063.1; -
DR HSP; P32965; 1CTL.
DR FlyBase; FBgn0014863; Mlp84B.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 5.
DR ProDom; PD000094; LIM; 5.
DR SMART; SM00132; LIM; 5.
DR PROSITE; PS00478; LIM DOMAIN 1; 5.
DR PROSITE; PS00023; LIM DOMAIN 2; 5.
KW Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis;
KW Developmental protein; Differentiation.
FT DOMAIN 12 63
FT DOMAIN 65 80
FT DOMAIN 66 71
FT DOMAIN 120 172
FT DOMAIN 175 180
FT DOMAIN 178 189
FT DOMAIN 222 274
FT DOMAIN 276 291
FT DOMAIN 325 377
FT LIM 1.
FT GLY-RICH.
FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT LIM 2.
FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT GLY-RICH.
FT LIM 3.
FT GLY-RICH.
FT LIM 4.

FT DOMAIN 379 390
FT DOMAIN 421 473
FT DOMAIN 475 490
SQ SEQUENCE 495 AA; 53525 MW; 2E559B9178E54C0E CRC64;
Query Match 11.4%; Score 69.5; DB 1; Length 495;
Best Local Similarity 28.0%; Pred.No.16; 7; Mismatches 15; Gaps 2;
Matches 23; Conservative
QY 20 ALLRVSAGVQAP-----GTAPCRSGSGSWADLDKCMDKAS-----CRARPHSDFC 64
Db 110 ATATAPGEGPCRCGCVVVAEEQLAGRSWHKECFKCGTCKGLDGLDILCCAPDKNIYC 169
QY 65 LGCAAPAPAPFRLWLLPILGAL 86
Db 170 KGYAKKFGPKGYGGGGGAL 191
RESULT 15
PTTG_HUMAN STANDARD; PRT; 180 AA.
ID PTTG_HUMAN
AC P53801; Q9NS09;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pituitary tumor-transforming gene 1 protein-interacting protein
DE (Pituitary tumor-transforming gene protein binding factor) (PTTG-
DE binding factor) (PBF).
GN PTTG1IP OR C21ORF1 OR C21ORF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=98234553; PubMed=9570958;
RA Yaspo M.-L., Aaltonen J., Horelli-Kuitunen N., Peltonen L.,
RA Lehtirach H.;
RT "Cloning of a novel human putative type Ia integral membrane protein
RT mapping to 21q22.3.";
RL Genomics 49:133-136(1998).
RN [2]
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND INTERACTION WITH PTTG1.
RX MEDLINE=20317150; PubMed=10781616;
RA Chien W., Pei L.;
RT "A novel binding factor facilitates nuclear translocation and
RT transcriptional activation function of the pituitary
RT tumor-transforming gene product.";
RL J. Biol. Chem. 275:19422-19427(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloesker H.,
RA Rammer J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehtirach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, Lung, Muscle, and Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,

Search completed: March 1, 2004, 16:43:01
Job time : 19 secs

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May facilitate PTTGI nuclear translocation.
CC -!- SUBUNIT: Interacts with PTTGI.
CC -!- SUBCELLULAR LOCATION: According to Ref.2, it is found in the
CC cytoplasm and in the nucleus. According to Ref.1, it is a type I
CC membrane protein.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL; Z50022; CAA90325.1; -
DR EMBL; AF149785; AAF73770.1; -
DR EMBL; AL163300; CAB90552.1; -
DR EMBL; BC000435; AAH00435.1; -
DR EMBL; BC012858; AAH12858.1; -
DR EMBL; BC019295; AAH19295.1; -
DR EMBL; BC020983; AAH20983.1; -
DR EMBL; BC031097; AAH31097.1; -
DR EMBL; BC034250; AAH34250.1; -
DR Genew; HGNC:13524; PTTGLIP.
DR MIM; 603784; -
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0016020; C:membrane; NAS.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0006006; P:protein-nucleus import; IDA.
DR InterPro; IPR003659; P:protein-like.
DR SMART; SMO0423; PSI; 1.
DR Transmembrane; Nuclear protein.
KW TRANSMEM 97 117 POTENTIAL.
FT DOMAIN 116 121 POLY-CYS.
FT CONFLICT 9 19 PTPVRLRLGG -> ARHTGGCASV (IN REF. 2).
FT CONFLICT 108 114 TLLGIA -> NPPPGHC (IN REF. 2).
SQ SEQUENCE 180 AA; 20323 MW; FIE66014D49ECIDE CRC64;

Query Match 11.3%; Score 69; DB 1; Length 180;
Best Local Similarity 25.8%; Pred. No. 6.9;
Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;

QY 10 LRLVLGLWLLALLRSVAGEAPGTAPCRSGSSWSADLDKCMDCASCRAPHSDFCLG--- 66
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
15 LRLGGAALLLLIPVAAAQEPFGAA-CSQNTKTC--EECLKNVSCSLWCNTNKACLDYFV 71
QY 67 CAAPAPAP-----PRLM-----PILGGALSLTFLGLSLGSLVWRRCRER 108
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
72 TSLVLPASLCKLSSARWGVCWNFEALITWSVGG-----TLLGI--AICCCCCRRKR 125
QY 109 SSPP 112
DB |||
126 SRKP 129
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 16:40:19 ; Search time 40 Seconds
(without alignments)
899.227 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRLRLVLGLMLA.....LSGFLVWRRCRRSSPPXP 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	453	74.5	129	11 Q80XX9	Q80xx9 rattus norv
2	87	14.3	333	4 Q9BZG3	Q9bzg3 homo sapien
3	87	14.3	426	4 Q9BZG2	Q9bzg2 homo sapien
4	83.5	13.7	610	10 Q943G8	Q943g8 oryza sativ
5	79.5	13.1	377	16 Q82N80	Q82n80 streptomyce
6	79	13.0	341	6 Q9N0B3	Q9n0b3 macaca fasc
7	78.5	12.9	332	10 Q42839	Q42839 hordeum vul
8	78.5	12.9	387	11 Q8VD70	Q8vd70 mus musculu
9	77.5	12.7	219	11 Q8BM15	Q8bm15 mus musculu
10	77.5	12.7	1208	11 Q80YA8	Q80ya8 mus musculu
11	76.5	12.6	245	16 Q8Z5R3	Q8z5r3 salmonella
12	76.5	12.6	732	16 Q81ZX4	Q81zx4 streptomyce
13	75.5	12.4	222	12 Q9QEE6	Q9qee6 indian citr
14	75.5	12.4	436	16 Q7U2G8	Q7u2g8 mycobacteri
15	75.5	12.4	449	16 Q53668	Q53668 mycobacteri
16	75.5	12.4	635	5 Q18288	Q18288 caenorhabdi

Q96kn9 homo sapien
Q8cxg1 oceanobacil
Q80mp4 indian citr
Q860w5 mus musculu
Q9a9x4 caulobacter
P90890 caenorhabdi
Q82fa3 streptomyce
Q9p2p7 homo sapien
Q04393 hordeum vul
Q8pqq6 xanthomonas
Q8n2r7 homo sapien
Q98th8 cyprinus ca
Q96qa0 homo sapien
Q8unc0 corynebacte
Q9nqd2 homo sapien
Q9rsc0 deinococcus
Q9y288 homo sapien
Q9b2w8 homo sapien
Q7wx79 alcaligenes
Q9iar7 gallus gall
Q818v6 giardia lam
Q95054 homo sapien
Q9w393 oryza sativ
Q93072 hepatitis g
Q90631 baboon herp
Q9e255 streptomyce
Q7wr57 bordetella
Q7w290 bordetella
Q7vt68 bordetella

ALIGNMENTS

RESULT 1

Q80XX9 PRELIMINARY; PRT; 129 AA.
AC Q80XX9
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Type 1 transmembrane protein FN14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller A.M., Giegerich G.;
RT "FN14, TNFRSF12a";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY255102; AAP06753.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
SQ SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;

Query Match 74.5%; Score 453; DB 11; Length 129;
Best Local Similarity 76.1%; Pred. No. 1.9e-39;
Matches 86; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARGSLRLRLVLGLMLALLRSVAGEQAPGTCPSRGSSWSADLDCMDCASCRRPH 60
DB 1 MAPGWPRFLPQLVLGLVLRATAGEQAPGNAFCSSGSSWSADLDCMDCASCRRPH 60
QY 61 SDFCLGCAAAAPAPRLLWPILGGLSITFVLGLSGFLVWRRCRRSSPPXP 113
DB 61 SDFCLGCAAAAPAPRLLWPILGGLSITFVLGLSGFLVWRRCRRRCRREKFTTP 113

RESULT 2

Q9BZG3 PRELIMINARY; PRT; 333 AA.
AC Q9BZG3

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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Acid phosphatase variant 3.
GN ACPT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309073; PubMed=11414767;
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
RT is highly expressed in the testis.";
RL Genomics 74:385-395(2001).
DR EMBL; AF321918; AAK09393.1; -.
DR HSSP; P15309; 2HPA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc phosphatase.
DR Pfam; PF00328; acid phosphat. 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;

Query Match 14.3%; Score 87; DB 4; Length 333;
Best Local Similarity 35.3%; Pred. No. 0.49;
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

Qy 31 PG-TAPCSGSSWADLCKMDCASCARPHSDFLCGLG-AAAPAPFRLIWPILGALS 87
Db 258 PGCFACPLGRFFYQL-----TAPARPPAHGVSCHGPYEAAPPAP---VVPILAGAVA 307
Qy 88 LTFVLGLSLGFLVWR-RCRERSRP 111
Db 308 VLVALSLGLGLLAWPGCLRALGPP 332

RESULT 3
QyBZG2 PRELIMINARY; PRT; 426 AA.
AC QyBZG2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Acid phosphatase.
GN ACPT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309073; PubMed=11414767;
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
RT is highly expressed in the testis.";
RL Genomics 74:385-395(2001).
DR EMBL; AF321918; AAK09393.1; -.
DR HSSP; P15309; 2HPA.
DR Genew; HGNC:14376; ACPT.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc phosphatase.
DR Pfam; PF00328; acid phosphat. 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 426 AA; 46089 MW; BE930398041DB061 CRC64;

Query Match 14.3%; Score 87; DB 4; Length 426;
Best Local Similarity 35.3%; Pred. No. 0.62;
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

Qy 31 PG-TAPCSGSSWADLCKMDCASCARPHSDFLCGLG-AAAPAPFRLIWPILGALS 87

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Db 351 PGCFACPLGRFFYQL-----TAPARPPAHGVSCHGPYEAAPPAP---VVPILAGAVA 400
Qy 88 LTFVLGLSLGFLVWR-RCRERSRP 111
Db 401 VLVALSLGLGLLAWPGCLRALGPP 425

RESULT 4
QyBZG2 PRELIMINARY; PRT; 610 AA.
AC QyBZG2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative receptor protein kinase.
DE P0046E05.12.
GN P0046E05.12.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0046E05.12."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AP003237; BAB67305.1; -.
DR Gramene; Q943G8; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR Pfam; PF00059; pkinase; 1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 610 AA; 64405 MW; 2A7B3EBE83FA9303 CRC64;

Query Match 13.7%; Score 83.5; DB 10; Length 610;
Best Local Similarity 24.6%; Pred. No. 2;
Matches 34; Conservative 12; Mismatches 35; Indels 57; Gaps 4;

Qy 30 APTAPCSGSSWADLCKMD-----CASCARPHSDP 63
Db 84 SPGDSSYTGSSSTSAIVTASTADPNAGDAVPTSGDAIPSSACRPAARCNRAFD- 142
Qy 64 CLGCAAPAPAPFRLIWP-----ILGALSLTFVLGLSLG- 97
Db 143 --NVPAAPPPPRISLSPPPPPTPTQSGASSGSSKSNNGTIVAVGVAAVVLGLAAGL 200
Qy 98 --FLVWRRCRRERSRSPPP 113
Db 201 IYFFVSKRRRRRQHPPPP 218

RESULT 5
QyBZG2 PRELIMINARY; PRT; 377 AA.
AC QyBZG2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.

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GN SAV1423.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis; deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005026; HAC69133.1; -.
DR InterPro; IPR007016; Wzy_C.
DR Pfam; PF04932; Wzy_C; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 377 AA; 36860 MW; 7964E23DFE6F29AA CRC64;
SQ
Query Match 13.1%; Score 79.5; DB 16; Length 377;
Best Local Similarity 34.1%; Pred. No. 3.3;
Matches 29; Conservative 10; Mismatches 33; Indels 13; Gaps 3;
QY 15 LGIWLALRSVAGEQAGTAPCSRGSSWSADLCKMDCASCRRPHSDFCLGCAAPPAP 74
Db 110 LGIWLALRSVAGEQAGTAPCSRGSSWSADLCKMDCASCRRPHSDFCLGCAAPPAP 74
QY 75 FLLWILGALSLT-FVGLISGF 98
Db 158 SRLALRLAAITVTAALGSLTGF 182
RESULT 6
Q9NOB3 PRELIMINARY; PRT; 341 AA.
AC Q9NOB3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unnamed protein product (Gap junction protein) (Connexin).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL
CC (BY SIMILARITY).
CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.
DR EMBL; AB046017; BAB01599.1; -.
GN GO:0005922; C:connexon complex; IEA.
GN GO:0016021; C:integral to membrane; IEA.
GN GO:0015285; F:connexon channel activity; IEA.
GN GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
SQ SEQUENCE 341 AA; 36784 MW; 4A71DEA938F0FA0C CRC64;
Query Match 13.0%; Score 79; DB 6; Length 341;
Best Local Similarity 27.9%; Pred. No. 3.4;
Matches 29; Conservative 9; Mismatches 46; Indels 20; Gaps 1;
QY 9 LRLVLGLWLLALRSVAGEQAGTAPCSRGSSWSADLCKMDCASCRRPHSDFCLGCA 68
Db 119 LRLVLGLWLLALRSVAGEQAGTAPCSRGSSWSADLCKMDCASCRRPHSDFCLGCA 68
QY 69 AAPAPPFRLWFLGGLSLTFLVGLISGLFVWRRCRERSPP 112
Db 159 VSRPTEKSLMLFLWAVSALSFLGLADLVCSLRRLRRRPGPP 202
RESULT 7
Q42839 PRELIMINARY; PRT; 332 AA.
ID Q42839;
AC Q42839;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chitinase (EC 3.2.1.14).
GN CHI33.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed.
RX MEDLINE=95078949; PubMed=7987416;
RA Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,
RA Mundy J.;
RT "Identification of an enhancer/silencer sequence directing the
RT aleurone-specific expression of a barley chitinase gene.";
RL Plant J. 6:579-589(1994).
DR EMBL; L34211; AAA56787.1; -.
DR FIR; T04484; T04484.
DR HSP; P23951; 2BAA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008843; F:endochitinase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR001002; Chitin binding.
DR InterPro; IPR00726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin bind_1; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase.
SQ SEQUENCE 332 AA; 35369 MW; 1B38554F49AC9E0F CRC64;

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Query Match      12.9%; Score 78.5; DB 10; Length 332;
Best Local Similarity 32.0%; Pred. No. 3.7;
Matches 33; Conservative 9; Mismatches 38; Indels 23; Gaps 7;

QY 13 LVGLMIALRSV-----AGEAPQ-TAP-----CSRSSWSADLDKMDCAKCRARPHSDF 63
DB 13 IVLSAALAMVMVRAQCGSQAGGATCNCCLCCSRFGYCGSTDYC--GAGCQSQ----- 65
QY 64 CLGCAAPAPFRLLPILGALSFLVGLLSGLFVWR-RCR 105
DB 66 CSGCGPTPPGSP-----GGVSSIISRLDFEQLLHRRDCQ 102

RESULT 8
Q8VD70
ID Q8VD70 PRELIMINARY; PRT; 387 AA.
AC Q8VD70;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2003 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 12.
GN TNFRSF25 OR TNFRSF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017526; AAH17526.1; -.
DR MGD; MGI:1934667; Tnfrsf25.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00305; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match      12.9%; Score 78.5; DB 11; Length 387;
Best Local Similarity 18.9%; Pred. No. 4.3;
Matches 35; Conservative 21; Mismatches 44; Indels 85; Gaps 7;

QY 4 GSJRLRLVLGLWIALRSVAGE-----QA 30
DB 18 GSTARVLQLFLPLLLLLLLLLLGGQGGSGRCDKASQKRYGPPCCRCPCRGHYMKA 77
QY 31 PGTAFC-----SRGSSWSADLDKMDC-----ASCRARP-----HS 61
DB 78 PCAEPGNSTCLPCPSDTFLTRDNHFKTDCTRCQVDEEMALQVLENCSAKSDTHCCQS 137
QY 62 DFLGCAAP-----PAPFLLWPIGGALSFLVGL--LLSGFLV 100
DB 138 GWCVDCTSTPCGKSPFCVPCGATTPVHEAPTLFW--VQVLGVAFLGAILICAYCR 195
QY 101 WRCR 105
DB 196 WQPCCK 200

RESULT 9
Q8BM15
ID Q8BM15 PRELIMINARY; PRT; 219 AA.

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AC Q8BM15;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Weakly similar to neurogenic locus notch 3 protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK031068; BAC27237.1; -.
DR PIR; PT0633; PT0633.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 2.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00179; EGF CA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF 1; 4.
DR PROSITE; PS01186; EGF 2; 2.
FT NON TER 1
SQ SEQUENCE 219 AA; 23098 MW; 9F2C4BB237F9B522 CRC64;

Query Match      12.7%; Score 77.5; DB 11; Length 219;
Best Local Similarity 30.0%; Pred. No. 3.2;
Matches 30; Conservative 16; Mismatches 45; Indels 9; Gaps 4;

QY 19 LALLRSVAGEQAPGTAPCSRGSSW--SADLDKMDCAKCRARPHSDFCLGCAAP-PAPF 75
DB 99 LAGLRCCSLDKPCASPCNLGGTCRVASGIFEC----TCSAGFSQGFCEVVKTLPLPLPF 154
QY 76 RLFWPIGGALS--LTFVLGSLSGFLVWRRCRRSSPPP 113
DB 155 PLLEVAVPACACLLLLLLLGLSLAARKRQSGCTYSP 194

RESULT 10
Q80YA8
ID Q80YA8 PRELIMINARY; PRT; 1208 AA.
AC Q80YA8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 5930402A21 protein (Fragment).
GN 5930402A21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M., Baker S., Basham D., Brooks K., Chillingworth T., Connor P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moulle S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whithead S., Barrrell B.G.;

"Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.";

Nature 413:848-852(2001).

[2]

SEQUENCE FROM N.A.

STRAIN=ty2 / ATCC 700931;

MEDLINE=22531367; PubMed=12644504;

Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodyonianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of *Salmonella enterica* serovar Typhi strains Ty2 and CT18.";

J. Bacteriol. 185:2330-2337(2003).

EMBL; AL627272; CAD05727.1; -

EMBL; AEO16837; AAC68576.1; -

GO; GO:0019861; C:flagellum; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0009306; P:protein secretion; IEA.

InterPro; IPR005837; FlpP.

InterPro; IPR005838; TypeIII_P.

Pfam; PF00813; FlpP; 1.

PRINTS; PR01302; TYPE3IMPPROT.

ProDom; PD002586; TypeIII_P; 1.

TIGRfam; TIGR01103; flfP; 1.

PROSITE; PS01060; FLIP_1; 1.

PROSITE; PS01061; FLIP_2; 1.

Flagellum; Complete proteome.

SEQUENCE 245 AA; 26755 MW; C9B9931F0653A4D4 CRC64;

Query Match 12.6%; Score 76.5; DB 16; Length 245;

Best Local Similarity 30.8%; Pred. NO. 4.5;

Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps

QY 6 LRRLLLVGLWGLLRVSAGEAPG--TAP-CSRGSSWSADLQKMDASCARP--- 59

Db 1 MRRLFLSLAGLW--LFSPAAALQLPELISQPLAGGQGSWSVQTLFTITLFLPAL 58

QY 60 --HSDF-----CLGCAAAAPPAPFRLIWLPILGALSLITFVL 92

Db 59 LMTSFTRIIIVGLRNALGTSAPPNOV----LLGLALFLITFPI 100

RESULT 12

Q81ZX4 PRELIMINARY; PRT; 732 AA.

AC Q81ZX4;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Putative serine/threonine protein kinase.

GN PKN16 OR SAV4717.

OS Streptomyces avermitilis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=33903;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

RK MEDLINE=21477403; PubMed=11572948;

RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

RT "genome sequence of an industrial microorganism *Streptomyces avermitilis*: deducing the ability of producing secondary metabolites.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).

RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RA MEDLINE=22608306; PubMed=12692562;
RX Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005040; BAC7429.1; -.
DR GO; GO:000524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002372; Bac_PQ_repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01011; PQ; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00564; PQ; 6.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase; Complete proteome.
SQ SEQUENCE 732 AA; 76174 MW; 41E6556B3D5EA722 CRC64;

Query Match 12.6%; Score 76.5; DB 16; Length 732;
Best Local Similarity 29.2%; Pred. No. 13;
Matches 35; Conservative 12; Mismatches 36; Indels 37; Gaps 7;

Q 2 ARGSLRRLRLVLGLWLLALRSVAGE---QAPGT-APCPSRGSS-----W-----SAD 45
338 ARKRLGR--RLWIPAVAVAVLACVAGLVLLGPGTGAPREQDAAPSKAAPQPDIGLSAG 395
Q 46 LDKMDCASCARPHSDRC-----LGCRAAPAPFRLW-----PILGGAL 86
396 GSKATGMAQCAYPHRLYCTPRGVLAATAVDADGKVLMSRGDAKRHSDGTVRPPVLGG 455

RESULT 13
Q9QEE6 PRELIMINARY; PRT; 222 AA.
AC Q9QEE6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 23kDa protein (Putative 23 kDa nucleic acid binding protein).
OS Indian citrus ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage.
OX NCBI_TaxID=104664;
RN [1]
RC STRAIN=K1.
RX MEDLINE=20496665; PubMed=11043949;
RA Rustici G., Accotto G.P., Norris E., Masenga V., Luisoni E.,
RA Milne R.G.;
RT "Indian citrus ringspot virus: a proposed new species with some
RT affinities to potex-, carla-, fovea- and alexiviruses.";
RL Arch. Virol. 145:1895-1908(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RA Rustici G., Milne R.G., Accotto G.P.;
RT "Nucleotide sequence, genome organization and phylogenetical analysis
RT of Indian citrus ringspot virus.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184962; AAF01314.1; -.
DR EMBL; AF406744; AAK97527.1; -.

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DR InterPro; IPR008891; Viral_NABP.
DR Pfam; PF05515; Viral_NABP; 1.
SQ SEQUENCE 222 AA; 25455 MW; 636A47058DD8D01D CRC64;

Query Match 12.4%; Score 75.5; DB 12; Length 222;
Best Local Similarity 35.4%; Pred. No. 5.2;
Matches 35; Conservative 7; Mismatches 38; Indels 19; Gaps 7;

Q 3 RGSRLRLRLVLGLWLLALRSVAGEQAP-GTAPCSRGSSWSADLDKMCASCRA--RP 59
21 RGSQIRSVRLLP---WRPFTFRFPV---CPSGTSPYSRGTHSQPSYVRQCERARQWFA 74
Q 60 H-SDFCL-----GCAAAPAPFRL--WPILGGALSL 88
75 HDGPRCLHQRPDYSRLQAPDPDQHLNLFEPILLALSV 113

RESULT 14
Q7U2G8 PRELIMINARY; PRT; 436 AA.
AC Q7U2G8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable conserved integral membrane protein.
GN MB0252.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RA MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248334; CAD93116.1; -.
KW Complete proteome.
SQ SEQUENCE 436 AA; 45353 MW; 1A2AB43B1052F07B CRC64;

Query Match 12.4%; Score 75.5; DB 16; Length 436;
Best Local Similarity 23.0%; Pred. No. 9.9;
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;

Q 1 MARGSLRRLRLVLGLWLLALRSVAGEQA--FGTAPCSRGSS--WSADLDKMCASCRA 56
142 MPSTAGARILLTEVGVAALTAVVAATLSFVDPDHPLSRNHLLWTAAVAMAISAACR 201
Q 57 ARPHSDFCLGCAAPAPFRLW-----PILGG----- 84
202 ALPHR--IVPRVHAAPGLHKLVTYVGTWTAITNGWYRYLLVQLVFGSVLGGSHSRVA 259
85 -----ALSLTFVLGLLGLFVLRRCR 105
260 AVPGDQDEVVAVVLFVCVGLLGLALWNRVR 291

RESULT 15
O53668 PRELIMINARY; PRT; 449 AA.
AC O53668;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative membrane protein.
GN RV0246 OR MTU0260 OR MV034.12.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021929; CAA17338.1; ALT_INIT.
DR EMBL; AE006934; AAK44478.1; -.
DR PIR; B70939; B70939.
DR TIGR; MT0260; -.
DR TuberculList; Rv0246; -.
KW Complete proteome.
SQ SEQUENCE 449 AA; 46926 MW; FCE6EF930F03D1E6 CRC64;
Query Match 12.4%; Score 75.5; DB 16; Length 449;
Best Local Similarity 23.0%; Pred. No. 10;
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;
QY 1 MARGSLRLRLRLVGLWLLRSVAGEQA--PCTAPCSRGS--WSADLDKMDCASCR 56
Db 155 MPSTARARILLTEVGVGAALTAVVAATLSFVPDQHLSRNHLLMTAAVMAISAICR 214
QY 57 ARHSDFCGLGCAAPAPPFRLLW-----PILGG----- 84
Db 215 ALPHR--IVPRVHAAPGLHKLIVYVGTARTNGWYRYLLVQVLFQSVVLGSSFSHSIRVA 272
QY 85 -----ALSLTFVLGLSLGFLVWRRCR 105
Db 273 AVPDQDPDEVVAVVLFVCVGLGLGIALWNRVR 304

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Search completed: March 1, 2004, 16:43:54
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:32:18 ; Search time 40 Seconds
(without alignments)
452.371 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRRLRLVGLWLA.....LSGFLVWRCRRERSPPPX 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 19Jun03.*

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1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	99.8	114	20	AAW73409 Human secreted pro
2	571	93.9	129	20	AAW88506 Human liver clone
3	571	93.9	129	21	AAV57940 Human transmembran
4	571	93.9	129	22	AAU03498 Human TWEAK recept
5	571	93.9	129	23	ABP61512 Human NF-kB activa
6	571	93.9	129	23	AAU79827 Human type 1 trans
7	571	93.9	129	24	ABU56716 Lung cancer-associ
8	450	74.0	129	23	AAU79828 Mouse type 1 trans
9	433	71.2	309	22	AAU03500 Human TWEAK recept

10	274.5	45.1	112	21	AAV91463 Human secreted pro
11	274.5	45.1	155	21	AAV91604 Human secreted pro
12	274.5	45.1	156	21	AAV91552 Human secreted pro
13	94.5	15.5	185	23	AAE22289 Human BAF receptor
14	92.5	15.2	185	23	AAE22266 Human BAF receptor
15	92.5	15.2	185	23	AAE22267 Human BAF receptor
16	91.5	15.0	185	23	AAE22270 Human BAF receptor
17	91.5	15.0	185	23	AAE22271 Human BAF receptor
18	89.5	14.7	185	23	AAE22268 Human BAF receptor
19	88.5	14.6	185	23	AAE22242 Human mature JST57
20	88.5	14.6	1388	23	ABP70117 Human NOV31a. Hom
21	88.5	14.6	1388	23	ABP70118 Human NOV31b. Hom
22	87	14.3	184	23	ABB81483 Human Znf112 prot
23	87	14.3	184	24	AAE35227 Human Znf112 rece
24	87	14.3	184	24	ABP97721 Amino acid sequenc
25	87	14.3	266	23	AAE22243 Human JST576 (BAFF
26	87	14.3	333	23	ABG32546 Human testicular a
27	87	14.3	375	23	ABG32542 Human testicular a
28	87	14.3	426	22	ABG32348 Novel human diagno
29	87	14.3	426	23	ABG32341 Human testicular a
30	87	14.3	426	23	AAU75788 Human protein phos
31	87	14.3	426	23	AAU09880 Novel human secret
32	80.5	13.2	426	21	AAH01337 TNF receptor apopt
33	80.5	13.2	508	16	AAH80631 2B10 AMH-receptor.
34	79	13.0	224	22	AAH95174 Human protein sequ
35	79	13.0	224	24	ABR01798 Human cancer-relat
36	77	12.7	152	22	ABG26293 Novel human diagno
37	77	12.7	448	21	AAV56750 Smooth muscle prol
38	77	12.7	448	21	AAV54990 Full length mouse
39	76.5	12.6	250	21	AAV58208 Canine mature Flt-
40	76.5	12.6	276	21	AAV58207 Canine Flt-3 ligan
41	76	12.5	141	22	AAW79666 Human protein SEQ
42	75	12.3	356	23	ABJ10913 Human secreted pro
43	75	12.3	356	23	ABF60987 Novel human protei
44	75	12.3	370	23	ABF60986 Novel human protei
45	74	12.2	234	22	AAW24485 Human EST encoded

ALIGNMENTS

RESULT 1
AAW73409
ID AAW73409 standard; Protein; 114 AA.
XX AC AAW73409;
XX DT 19-FEB-1999 (first entry)
XX DE Human secreted protein encoded by Gene No. 13.
DE DE Secreted protein; human; protein therapy; gene therapy; blood disorder;
KW pathologic condition; human; diagnosis; cancer; neurological disorder;
KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
KW immune system disorder; Alzheimer's disease; cognitive disorder;
KW schizophrenia; prostate disease; autoimmune disorder; AIDS.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Misc-difference 114
FT FT /note="unspecified amino acid"
XX PN WO9854206-A1.
XX PD 03-DEC-1998.
XX PF 28-MAY-1998; 98WO-US10868.
XX PR 29-AUG-1997; 97US-0056296.
XX PR 30-MAY-1997; 97US-0044039.
XX PR 30-MAY-1997; 97US-0048093.
XX PR 30-MAY-1997; 97US-0048101.

PR 30-MAY-1997; 97US-0048190.
 PR 30-MAY-1997; 97US-0048356.
 PR 30-MAY-1997; 97US-0050935.
 PR 29-AUG-1997; 97US-0056250.
 PR 29-AUG-1997; 97US-0056293.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Carter KC, Dillon PJ, Endress GA, Feng P, Ni J;
 PI Rosen CA, Ruben SM, Yu G;
 XX
 DR WPI; 1999-070209/06.
 DR N-PSDB; AAV08823.
 XX
 XX New isolated human genes - useful for diagnosis and treatment of,
 PT e.g. cancers, neurological disorders, immune diseases, developmental
 PT disorders or blood disorders
 XX
 XX Claim 11; Page 153; 188pp; English.
 PS
 CC This sequence is encoded by a cDNA of the invention, designated
 CC Gene No. 13. This sequence represents a human secreted protein, and is
 CC expressed in keratinocytes and to a lesser extent in endothelial
 CC cells and placenta.
 CC The DNA sequences of the invention and their corresponding secreted
 CC polypeptides are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the DNA sequences.
 CC Specific uses are described for each of the DNA sequences and the encoded
 CC proteins, based on which tissues they are most highly expressed in, and
 CC include developing products for the diagnosis or treatment of cancer,
 CC tumours, neurological disorders, developmental abnormalities and foetal
 CC deficiencies, blood disorders, leukaemias, diseases of the immune system
 CC (including allergies or asthma), hepatic disease, Alzheimer's and
 CC cognitive disorders, schizophrenia, prostate diseases, autoimmune
 CC disorders and AIDS. The polypeptides are also useful for identifying
 CC their binding partners.
 XX
 SQ Sequence 114 AA;
 Query Match 99.8%; Score 607; DB 20; Length 114;
 Best Local Similarity 100.0%; Pred. No. 6.5e-56;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARGSLRLLRLVLGLLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
 Db 1 MARGSLRLLRLVLGLLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
 QY 61 SDFCLGCAAAPAPPRLLWPILGGALSLTFVLGLSGFLVWRRCRERSPPPP 113
 Db 61 SDFCLGCAAAPAPPRLLWPILGGALSLTFVLGLSGFLVWRRCRERSPPPP 113
 RESULT 2
 AAW88506
 ID AAW88506 standard; Protein; 129 AA.
 XX
 AC AAW88506;
 XX
 DT 30-MAR-1999 (first entry)
 XX
 DE Human liver clone HP10432-encoded membrane protein.
 XX
 KW Transmembrane protein; HP10432; human; liver.
 XX
 OS Homo sapiens.
 XX
 PN WO9855508-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 03-JUN-1998; 98WO-JP02445.

XX 03-JUN-1997; 97JP-0144948.
 PR (PROT-) PROTEGENE INC.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 XX
 XX Kato S, Sekine S, Yamaguchi T;
 PI
 XX WPI; 1999-045730/04.
 DR N-PSDB; AAV84374.
 XX
 XX New human proteins containing transmembrane domains and their
 PT encoding sequences - useful in the preparation of antibodies and
 PT large-scale protein production, gene diagnosis, and gene therapy
 XX
 XX Claim 1; Page 152-153; 178pp; English.
 PS
 CC This is the amino acid sequence of a transmembrane protein encoded
 CC by human liver cDNA clone HP10432 (see AAV84374). The encoded protein
 CC has a signal-like N-terminal region and one internal transmembrane
 CC domain. The invention provides nucleotide sequences (see AAV84359-76)
 CC coding for 18 transmembrane proteins (see AAV84391-508), vectors
 CC containing such polynucleotides, and eukaryotic cells containing the
 CC vectors. The proteins can be used as antigens or as compositions
 CC in the preparation of antibodies against the proteins. The
 CC polynucleotides can be used as probes for gene diagnosis, and as
 CC gene sources for gene therapy and large-scale production of proteins
 CC encoded by the cDNA. The host cells are used for the detection of
 CC ligands corresponding to the expressed proteins, and the screening
 CC of low mol.wt. medicines.
 XX
 SQ Sequence 129 AA;
 Query Match 93.9%; Score 571; DB 20; Length 129;
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MARGSLRLLRLVLGLLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
 Db 1 MARGSLRLLRLVLGLLWALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
 QY 61 SDFCLGCAAAPAPPRLLWPILGGALSLTFVLGLSGFLVWRRCRERSPPPP 113
 Db 61 SDFCLGCAAAPAPPRLLWPILGGALSLTFVLGLSGFLVWRRCRERSPPPP 113
 RESULT 3
 AAY57940
 ID AAY57940 standard; Protein; 129 AA.
 XX
 AC AAY57940;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human transmembrane protein HTMPN-64.
 XX
 KW Human; transmembrane protein; HTMPN; diagnosis; immunospecific;
 KW antiproliferative; neuroprotective; immune disorder;
 KW reproductive disorder; smooth muscle disorder; neurological disorder;
 KW gastrointestinal disorder; developmental disorder;
 KW cell proliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO9961471-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11904.
 XX
 PR 29-MAY-1998; 98US-0087260.
 PR 02-JUL-1998; 98US-0091674.
 PR 02-OCT-1998; 98US-0102954.

PR 24-NOV-1998; 98US-0109869.

PA (INCY-) INCYTE PHARM INC.

PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KU, Corley NC;
 PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;
 PI Au-Young J;

XX WPI: 2000-072605/06.

DR N-PSDB; AAZ56761.

XX Proteins, polynucleotides, vectors, host cells and antibodies used to
 PT diagnose, treat or prevent immune, reproductive, smooth muscle,
 PT neurological, gastrointestinal, developmental and cell proliferative
 PT disorders -

XX Claim 1; Page 163; 229pp; English.

XX AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human
 CC transmembrane proteins designated HTPN-1 to HTPN-79, respectively.
 CC The transmembrane protein have immunospecific, antiproliferative and
 CC neuroprotective activities. The human transmembrane proteins,
 CC polynucleotides encoding them and other compositions and methods from
 CC the present invention, can be used for the diagnosis, treatment or
 CC prevention of immune, reproductive, smooth muscle, neurological,
 CC gastrointestinal, developmental and cell proliferative disorders. The
 CC HTPN's can be used to treat or prevent disorders associated with a
 CC decreased expression or activity of HTPN.

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 21; Length 129;

Best Local Similarity 94.7%; Pred. No. 4.4e-52;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 60

DB 1 MARGSLRRLRLVLGLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 60

QY 61 SDFCLGCAAPAPFRLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 113

DB 61 SDFCLGCAAPAPFRLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 113

RESULT 4

AAU03498
 ID AAU03498 standard; Protein; 129 AA.

XX AC AAU03498;

XX 26-SEP-2001 (first entry)

XX Human TWEAK receptor (TWEAKR) polypeptide.

XX TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
 KW rubeosis; uveitis; macular degeneration; arthritis; rheumatism;
 KW corneal graft neovascularisation; psoriasis; metastatic condition;
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;
 KW peripheral atherosclerosis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..27

XX /note= "Signal peptide"

XX Protein 28..129

XX /note= "Mature human TWEAKR protein"

XX Domain 1..78

FT Domain /note= "Extracellular domain"
 FT 79..101

FT Domain /note= "Transmembrane domain"
 FT 102..129

XX Domain /note= "Intracellular domain"

PN WO200145730-A2.

XX 28-JUN-2001.

XX 19-DEC-2000; 2000WO-US34755.

XX 20-DEC-1999; 99US-0172878.

XX 10-MAY-2000; 2000US-0203347.

XX (IMMV) IMMUNEX CORP.

XX Wiley SR;

XX WPI: 2001-417975/44.

XX N-PSDB; AAS03963.

XX Modulating angiogenesis in a mammal for treating diseases mediated by
 PT angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or
 PT peripheral tissue, by administering antagonist or agonist of TWEAK
 PT receptor -

XX Example 1; Fig 1; 46pp; English.

XX The sequence represents the human TWEAK receptor (TWEAKR) protein. The
 CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and
 CC induces angiogenesis. TWEAKR may therefore be used to screen for and
 CC develop TWEAKR agonists and antagonists for the modulation of
 CC angiogenesis, to be used in the treatment and diagnosis of human disease.
 CC The disorders mediated by angiogenesis include ocular disorders
 CC characterised by ocular neovascularisation such as diabetic retinopathy,
 CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity,
 CC retrolental fibroplasia, rubeosis, uveitis, macular degeneration and
 CC corneal graft neovascularisation, and inflammatory diseases such as
 CC arthritis, rheumatism and psoriasis. Other treatable diseases include
 CC malignant and metastatic conditions such as sarcomas and carcinomas,
 CC benign tumours and preneoplastic conditions, myocardial angiogenesis,
 CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic
 CC plaque neovascularisation, telangiectasia, wound granulation, coronary
 CC atherosclerosis, peripheral atherosclerosis and ischaemia.

XX Sequence 129 AA;

Query Match 93.9%; Score 571; DB 22; Length 129;

Best Local Similarity 94.7%; Pred. No. 4.4e-52;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLGLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 60

DB 1 MARGSLRRLRLVLGLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 60

QY 61 SDFCLGCAAPAPFRLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 113

DB 61 SDFCLGCAAPAPFRLWLLRSVAGEQAPGTAPCSRSGSSWADLDKMDCAACSCARPH 113

RESULT 5

ABP61512
 ID ABP61512 standard; Protein; 129 AA.

XX AC ABP61512;

XX 30-SEP-2002 (first entry)

XX Human NF-kB activating protein SEQ ID NO 178.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;

XX immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;

KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 XX bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
 KW Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP11389.

XX 28-DEC-2000; 2000JP-0402288.

XX 26-MAR-2001; 2001JP-0088912.

XX 24-AUG-2001; 2001JP-0254018.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI; 2002-583617/62.

XX N-PSDB; ABQ92000.

XX NF-approximatelyB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer -

XX Claim 4; Page 814-815; 841pp; Japanese.

XX The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-KB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition
 CC and for treating e.g. inflammations, autoimmune diseases, cancers,
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
 CC disorders.

SQ Sequence 129 AA;

Query Match 93.9%; Score 571; DB 23; Length 129;

Best Local Similarity 94.7%; Pred. No. 4.4e-52;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLDKMDCCASCARPH 60

DB 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLDKMDCCASCARPH 60

OY 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLGLFVWRCRRERSPPPP 113

DB 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLGLFVWRCRRERSPPPP 113

RESULT 6

AAU79827

ID AAU79827 standard; Protein; 129 AA.

XX AAU79827;

XX 15-JUL-2002 (first entry)

XX Human type 1 transmembrane protein Fn14.

XX Type 1 transmembrane protein Fn14; human; cytotstatic; cardiant;
 KW vulnerary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;
 KW tumour necrosis factor family; TNF family; TWEAK receptor;
 KW myocardial ischaemic condition; myocardial infarction; wound healing;
 KW burn healing; gastric ulcer; tissue transplantation;
 KW organ transplantation; neovascularisation; vascular insufficiency;
 KW cancer; inflammatory macular degeneration; diabetic retinopathy.

XX Homo sapiens.

XX WO200222166-A2.

XX 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US28451.

XX 14-SEP-2000; 2000US-232355P.

XX (BIOJ) BIOGEN INC.

XX Browning J, Burkly L, Jakubowski A, Zheng T;

XX WPI; 2002-383103/41.

XX Methods of modulating angiogenesis and inhibiting tumour progression,
 PT using TWEAK receptor agonists -

XX Disclosure; Fig 10A; 37pp; English.

XX The invention describes methods of modulating angiogenesis and inhibiting
 CC tumour progression using TWEAK (a novel member of the tumour necrosis
 CC factor or INF family) receptor agonists. Conditions which can be treated
 CC using the agonists include myocardial ischaemic conditions (e.g.
 CC myocardial infarction), wound healing (e.g. burn healing and healing of
 CC gastric ulcers), and tissue and organ transplantations to promote
 CC neovascularisation, particularly in subjects suffering from vascular
 CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and
 CC subsequently neovascularisation is useful in treatment of cancer,
 CC inflammatory macular degeneration and diabetic retinopathy. This sequence
 CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor
 CC described in the invention.

SQ Sequence 129 AA;

Query Match 93.9%; Score 571; DB 23; Length 129;

Best Local Similarity 94.7%; Pred. No. 4.4e-52;

Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLDKMDCCASCARPH 60

DB 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLDKMDCCASCARPH 60

OY 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLGLFVWRCRRERSPPPP 113

DB 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLGLFVWRCRRERSPPPP 113

RESULT 7

ABU56716

ID ABU56716 standard; Protein; 129 AA.

XX ABU56716;

XX 02-APR-2003 (first entry)

XX Lung cancer-associated polypeptide #309.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WO200296443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.

PR 10-MAY-2001; 2001US-290492P.
 PR 09-NOV-2001; 2001US-339245P.
 PR 13-NOV-2001; 2001US-350666P.
 PR 29-NOV-2001; 2001US-334370P.
 PR 12-APR-2002; 2002US-372246P.
 XX
 PA (SOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Aziz N, Murray R;
 XX
 XX WPI; 2003-093161/08.
 DR N-PSDB; ABX76445.
 XX

XX Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer -
 XX

XX Claim 27; Page 429; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung
 CC cancer-associated polynucleotides and polypeptides are used for
 CC identifying a compound that modulates a lung cancer-associated
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated
 CC cell to treat lung cancer in a patient and for treating a mammal having
 CC lung cancer by administering a modulatory compound identified. The
 CC methods are useful for treating lung cancer, such as small cell lung
 CC cancer, non-small cell lung cancer or other benign or precancerous
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
 CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
 CC polypeptides of the invention.
 XX

SQ Sequence 129 AA;

Query Match 93.9%; Score 571; DB 24; Length 129;
 Best Local Similarity 94.7%; Pred. No. 4.4e-52;
 Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLRLVGLWGLALLRSVAGEQAPGTAPCSRGSWSGADLDKMDCCASCARPH 60
 DB 1 MARGSLRLRLRLVGLWGLALLRSVAGEQAPGTAPCSRGSWSGADLDKMDCCASCARPH 60

QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGSLGFLVWRRCRERSPPPP 113
 DB 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGSLGFLVWRRCRERSPPPP 113

RESULT 8
 AAU79828

ID AAU79828 standard; Protein; 129 AA.

XX AC AAU79828;

XX 15-JUL-2002 (first entry)

DE Mouse type 1 transmembrane protein Fn14.

XX Type 1 transmembrane protein Fn14; mouse; cytostatic; cardiant;
 KW vlnutary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;
 KW tumour necrosis factor family; TNF family; TWEAK receptor;
 KW myocardial ischaemic condition; myocardial infarction; wound healing;
 KW burn healing; gastric ulcer; tissue transplantation;
 KW organ transplantation; neovascularisation; vascular insufficiency;
 KW cancer; inflammatory macular degeneration; diabetic retinopathy.
 XX

OS Mus musculus.

XX WO200222166-A2.

XX 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US28451.

XX 14-SEP-2000; 2000US-232355P.

XX (BIOJ) BIOGEN INC.

XX Browning J, Burkly L, Jakubowski A, Zheng T;

XX WPI; 2002-383103/41.

XX Methods of modulating angiogenesis and inhibiting tumour progression,
 PT using TWEAK receptor agonists -

XX Disclosure; Fig 10B; 37pp; English.

XX The invention describes methods of modulating angiogenesis and inhibiting
 CC tumour progression using TWEAK (a novel member of the tumour necrosis
 CC factor or TNF family) receptor agonists. Conditions which can be treated
 CC using the agonists include myocardial ischaemic conditions (e.g.
 CC myocardial infarction), wound healing (e.g. burn healing and healing of
 CC gastric ulcers), and tissue and organ transplantations to promote
 CC neovascularisation, particularly in subjects suffering from vascular
 CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and
 CC subsequently neovascularisation is useful in treatment of cancer,
 CC inflammatory macular degeneration and diabetic retinopathy. This sequence
 CC represents the mouse type 1 transmembrane protein Fn14, a TWEAK receptor
 CC described in the invention.

SQ Sequence 129 AA;

Query Match 74.0%; Score 450; DB 23; Length 129;

Best Local Similarity 75.2%; Pred. No. 2.1e-39;

Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARGSLRLRLRLVGLWGLALLRSVAGEQAPGTAPCSRGSWSGADLDKMDCCASCARPH 60

DB 1 MAPGWPRLPQIILVGLVLMRAAAGEQAPGTPCSRGSWSGADLDKMDCCASCARPH 60

QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGSLGFLVWRRCRERSPPPP 113

DB 61 SDFCLGCAAAAPPAPFRLLPILGGALSITFVLGSLGFLVWRRCRERSPPPP 113

RESULT 9
 AAU03500

ID AAU03500 standard; Protein; 309 AA.

XX AC AAU03500;

XX 26-SEP-2001 (first entry)

DE Human TWEAK receptor-Fc (TWEAKR-Fc) fusion polypeptide.

XX TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
 KW rubeosis; uveitis; macular degeneration; arthritis; rheumatism;
 KW corneal graft neovascularisation; psoriasis; metastatic condition;
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;
 KW peripheral atherosclerosis; human IgG1; TWEAKR-Fc; fusion protein.

OS Homo sapiens.

OS Synthetic.

XX

Query Match 45.1%; Score 274.5; DB 21; Length 112;
 Best Local Similarity 96.4%; Pred. No. 4.3e-21;
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKQDCAC-SC 55
 |||||
 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKQDCSTSC 56

Db

RESULT 11
 AAY91604
 ID AAY91604 standard; Protein; 155 AA.
 XX
 AC AAY91604;
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:277.
 XX
 KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
 KW antiHIV; antiinflammatory; nontropic; neuroprotective; antiallergic;
 KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
 KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
 KW immune disease; inflammation; blood disorder; tumour; chromosome 16.
 XX
 OS Homo sapiens.
 XX
 PN WO200006698-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 29-JUL-1999; 99WO-US17130.
 XX
 PR 30-JUL-1998; 98US-0094657.
 PR 05-AUG-1998; 98US-0095486.
 PR 06-AUG-1998; 98US-0095454.
 PR 06-AUG-1998; 98US-0095455.
 PR 12-AUG-1998; 98US-0096319.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
 PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
 PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
 XX
 DR WPI; 2000-195282/17.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Disclosure; Page 36-37; 634pp; English.
 XX
 CC The polynucleotide sequences given in AAY91604 encode the
 CC human secreted proteins given in AAY91604 to AAY91691. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: cytostatic;
 CC immunosuppressive; antiHIV; antiinflammatory; nontropic; neuroprotective;
 CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
 CC antiasthma; antipsoriatic; cardiant. The polynucleotides and their
 CC corresponding secreted proteins are useful for preventing, treating or
 CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
 CC pathological conditions can be diagnosed by determining the amount of the
 CC proteins in a sample or by determining the presence of mutations in the
 CC polynucleotides. Specific uses are described for each of the
 CC polynucleotides, based on which tissues they are most highly expressed
 CC in, and include developing products for the diagnosis or treatment of
 CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, hepatic and renal disease, inflammation.
 CC allergies, Alzheimer's and behavioural disorders, schizophrenia,
 CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,
 CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,

CC cardiovascular disorders, reproductive disorders, gastrointestinal
 CC disorders, respiratory disorders and metabolic disorders. The proteins
 CC or polynucleotides can also be used as food additives or preservatives.
 CC The proteins are also useful for identifying their binding partners.
 CC AAA26337 to AAA26345 and AAY91450 are sequences used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 155 AA;

Query Match 45.1%; Score 274.5; DB 21; Length 155;
 Best Local Similarity 96.4%; Pred. No. 6.1e-21;
 Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKQDCAC-SC 55
 |||||
 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKQDCSTSC 56

Db

RESULT 12
 AAY91552
 ID AAY91552 standard; Protein; 156 AA.
 XX
 AC AAY91552;
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:225.
 XX
 KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
 KW antiHIV; antiinflammatory; nontropic; neuroprotective; antiallergic;
 KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
 KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
 KW immune disease; inflammation; blood disorder; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200006698-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 29-JUL-1999; 99WO-US17130.
 XX
 PR 30-JUL-1998; 98US-0094657.
 PR 05-AUG-1998; 98US-0095486.
 PR 06-AUG-1998; 98US-0095454.
 PR 06-AUG-1998; 98US-0095455.
 PR 12-AUG-1998; 98US-0096319.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
 PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
 PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
 XX
 DR WPI; 2000-195282/17.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Claim 11; Page 528; 634pp; English.
 XX
 CC The polynucleotide sequences given in AAY91552 to AAY91691 encode the
 CC human secreted proteins given in AAY91552 to AAY91691. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: cytostatic;
 CC immunosuppressive; antiHIV; antiinflammatory; nontropic; neuroprotective;
 CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
 CC antiasthma; antipsoriatic; cardiant. The polynucleotides and their
 CC corresponding secreted proteins are useful for preventing, treating or
 CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
 CC pathological conditions can be diagnosed by determining the amount of the

proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. CC AAA26337 to AAA26345 and AAY91450 are sequences used in the exemplification of the present invention.

Sequence 156 AA;
Query Match 45.1%; Score 274.5; DB 21; Length 156;
Best Local Similarity 96.4%; Pred. No. 6.2e-21;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRLRLVLLGLWLLIRSVAGEQAPGTAPCSRGSSWSADLDKMDCA-SC 55
Db 1 MARGSLRLRLVLLGLWLLIRSVAGEQAPGTAPCSRGSSWSADLDKMDCTSC 56

RESULT 13
AAE22269
ID AAE22269 standard; Protein; 185 AA.

XX AC AAE22269;
XX DT 25-JUL-2002 (first entry)
XX DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.

XX KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
XX KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
XX KW Myasthenia gravis; hypertension; organ transplantation; drug screening;
XX KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
XX KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
XX KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
XX KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
XX OS Homo sapiens.

XX FT Key Location/Qualifiers
XX FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
XX FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
XX PN WO200224909-A2.

XX PD 28-MAR-2002.
XX PF 06-SEP-2001; 2001WO-US28006.
XX PF 18-SEP-2000; 2000US-233152P.
XX PR 21-SEP-2000; 2000US-234140P.
XX PR 13-FEB-2001; 2001US-268499P.
XX PR 14-AUG-2001; 2001US-312185P.

XX PA (BIOJ) BIOGEN INC.
XX XX Ambrose CM, Thompson JS;
XX DR WPI; 2002-362428/39.
XX PT New human BAFF receptor proteins and nucleic acids, useful for

PT treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal disorders -
XX Example 17; Page -; 164pp; English.
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumorigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal diseases, inflammation, organ transplantation and HIV. Autoimmune diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease, Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. CC The present sequence is human BAFF-R protein mutant.
CC Note: The present sequence is not shown in the specification but is derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the specification.

XX SQ Sequence 185 AA;
Query Match 15.5%; Score 94.5; DB 23; Length 185;
Best Local Similarity 27.8%; Pred. No. 0.053;
Matches 35; Conservative 13; Mismatches 39; Indels 39; Gaps 6;

Qy 23 RSVAGEQAPGTAPCSRGSSWSADLDKMDCA-RA-RPHSDFCIGCAAAAPPAPFLLWP- 80
Db 6 RSLRGDAPAPTONQAEFDLLVHVCAGLLTRPKP-AGNASSPAPRTALQPO 61
Qy 81 -----ILGGA---LSLTFLVGL-LSGFLVWRCRR-----E 107
Db 62 ESVGAGAGEAALPLPGLLFGAPALLGLALVLAIVLVGWSRRRRQRLRGASSAEPDGD 121
Qy 108 RSSPPP 113
Db 122 KDAPEP 127

RESULT 14
AAE22266
ID AAE22266 standard; Protein; 185 AA.
XX AC AAE22266;
XX DT 25-JUL-2002 (first entry)
XX DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P.

XX KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
XX KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
XX KW Myasthenia gravis; hypertension; organ transplantation; drug screening;
XX KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
XX KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
XX KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
XX KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
XX OS Homo sapiens.

cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BPFR antibodies, or in screening drugs or compounds that modulate BAPF-R activity or expression. The present sequence is human BAPF-R protein mutant.

Note: The present sequence is not shown in the specification but is derived from human BAPF-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the specification.

Sequence	185 AA;
SQ	

Query Match	15.2%;	Score	92.5;	DB	23;	Length	185;
Best Local Similarity	27.8%;	Pred. No.	0.086;				
Matches	35;	Conservative	13;	Mismatches	39;	Indels	39; Gaps
							6;
QY	23	RSVAGEQA	PCATPCSRCSSWSADLKCMDCASCR	A-RPHSDFCLGCAAAAPAFRLWP-	80		
Dd	6	RSURGRDAP	PTCNOTECDLLVRHCVAAGLLETPRPX	-AGAAASPAPRTALQPQ	61		
QY	81	-----ILGGA-	LSLITFVLGL-LSGFLVWRCCR	-----E	107		
Dd	62	ESVGAGAGEAALPLGLLFGCAPALLGLAVL	VLVLVLVLSWRRQRRLRGCSAEAPDG	121			
QY	108	RSSPPP	113				
Dd	122	KDAEP	127				

Search completed: February 11, 2004, 10:38:06
Job time : 41 secs

C:Function:

A:Description: may be involved in flagellar assembly; may be involved in export of flagellar biosynthetic protein flipp
 C:Superfamily: flagellar biosynthetic protein flipp
 C:Keywords: flagellum; transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <STG>
 F:122-245/Product: probable export protein flipp #status predicted <MAT>
 F:745-61/Domain: transmembrane #status predicted <TM1>
 F:189-105/Domain: transmembrane #status predicted <TM2>
 F:189-205/Domain: transmembrane #status predicted <TM3>
 F:212-228/Domain: transmembrane #status predicted <TM4>

Query Match 12.6%; Score 76.5; DB 2; Length 245;
 Best Local Similarity 30.8%; Pred. No. 4.3;
 Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRRLLRLVGLLWALLRSVAGEAPG--TAP-CSRGSWSADLDKMDKMDSCARCP--- 59
 DB 1 MRRLLFLSLAGLW--LFSFAAAQPLGLISQPLAGGQSWLSVOTLVFTSLTFLPAIL 58
 QY 60 --HSDF-----CLGCAAAAPPAPFRLLWPIILGALSLETVL 92
 DB 59 LMTSFTRIIVFGLLRNALGTPSPAPNQV-----LLGLALFLTFPI 100

RESULT 3

AD0753
 flagellar biosynthetic protein flipp [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: This species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AD0753
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, R.; Davies, R.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Aitken, C.
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 C:Accession: AD0753
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-245 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05727.1; PID:gl6503220; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY2187
 C:Superfamily: flagellar biosynthetic protein flipp

Query Match 12.6%; Score 76.5; DB 2; Length 245;
 Best Local Similarity 30.8%; Pred. No. 4.3;
 Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRRLLRLVGLLWALLRSVAGEAPG--TAP-CSRGSWSADLDKMDKMDSCARCP--- 59
 DB 1 MRRLLFLSLAGLW--LFSFAAAQPLGLISQPLAGGQSWLSVOTLVFTSLTFLPAIL 58
 QY 60 --HSDF-----CLGCAAAAPPAPFRLLWPIILGALSLETVL 92
 DB 59 LMTSFTRIIVFGLLRNALGTPSPAPNQV-----LLGLALFLTFPI 100

RESULT 4

B70939
 hypothetical protein B70246 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: B70939
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: B70939

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-436 <COL>
 A:Cross-references: GB:AL021929; GB:AL123456; NID:93242291; PIDN:CAA17338.1; PID:el2524;
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV0246

Query Match 12.4%; Score 75.5; DB 2; Length 436;
 Best Local Similarity 23.0%; Pred. No. 8.4;
 Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;

QY 1 MARGSLRLRLVGLLWALLRSVAGEQA--PCTAPCSRGS--WSADLDKMDKMDSCAR 56
 DB 142 MPSTAGARILLTEVGVAALTAVAATLSFVDPQHPLSRNILLTAAVAMA-SAAICR 201
 QY 57 ARPHSDFLCGLCAAAAPPAPFRLLW-----PIIGG----- 84
 DB 202 ALPHR--IVPRVHAAPGLHLYVVGWTAIRTNWYRRYLLVQVLFSGSVLGSSEHSIRVA 259
 QY 85 -----ALSITFVLGLSGFLVWRRCR 105
 DB 260 AVPGDQDEVVAVVLFVCGVLLGLLWNRVR 291

RESULT 5

T20910
 hypothetical protein ZK1010.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T20910; T27646
 R:McMurray, A.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19345
 A:Accession: T20910
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-635 <W11>
 A:Cross-references: EMBL:Z81503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9
 A:Experimental source: clone F14F7
 R:Gardner, A.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z20398
 A:Accession: T27646
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-635 <W12>
 A:Cross-references: EMBL:Z82083; PIDN:CAB04975.1; GSPDB:GN00021; CESP:ZK1010.9
 A:Experimental source: clone ZK1010
 C:Genetics:
 A:Gene: CESP:ZK1010.9
 A:Map position: 3
 A:Introns: 71/3; 184/2; 316/3; 403/1; 444/3; 547/3; 577/3
 C:Superfamily: gamma-aminobutyric acid transporter

Query Match 12.4%; Score 75.5; DB 2; Length 635;
 Best Local Similarity 36.6%; Pred. No. 11;
 Matches 26; Conservative 10; Mismatches 28; Indels 7; Gaps 3;

QY 31 PGTAPCSRGSWSADLDKMDKMDSCARCP--HSDFCLG--CAAAAPPAPFRLLWPIILGAL 86
 DB 92 PTTAYKRGGLSF---LTYVYVCGILFAVPAHMEFALGOVAAKSPPAFRMMPILEGVG 148
 QY 87 SLTTFVLGLSG 97
 DB 149 WMTCLVGAIG 159

RESULT 6

B97353
 hypothetical protein CC0837 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C;Accession: B87353
 R;Nieman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 D.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: B87353
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-519 <STO>
 A;Cross-references: GB:AE005673; NID:G13422090; PIDN:AAK22822.1; GSPDB:GN00148
 C;Genetics:
 A;Gene: CC0837

Query Match 12.3%; Score 74.5; DB 2; Length 519;
 Best Local Similarity 24.3%; Pred. No. 12;
 Matches 33; Conservative 21; Mismatches 51; Indels 31; Gaps 4;
 QY 9 LLRLVLGLMLLRS-VAGEQAPCTAPCSGRS-----SWSADLDKCMD 51
 Db 250 LLILMAGLGLFLFAAQVGLKRFADAAATGATRAAKGPGVCAFAAGAFQATLRKELR 309
 QY 52 CASCRARPHSDFCLGCAAAAPPAPRL-----WPILGALSILTEVLGLLGLVWRR 103
 Db 310 LVSRDAALLSQLRLVLMVPIAFVMVGRGSLPAWALAGFAAAVTFLAGQVAGSLIWI 369
 QY 104 CRRERS-----SPPP 113
 Db 370 VSAEDTPDLAISPSP 385

RESULT 7
 T22758
 hypothetical protein F55H12.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
 C;Accession: T22758
 R;Dobson, R.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z19610
 A;Accession: T22758
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-768 <WIL>
 A;Cross-references: EMBL:Z81091; PIDN:CA803142.1; GSPDB:GN00019; CRSP:F55H12.1
 A;Experimental source: clone F55H12
 C;Genetics:
 A;Gene: CRSP:F55H12.1
 A;Map position: 1
 A;Introns: 114/3; 189/1; 301/2; 426/3; 513/1; 554/3; 657/3; 687/3; 741/1
 C;Superfamily: gamma-aminobutyric acid transporter

Query Match 12.2%; Score 74; DB 2; Length 768;
 Best Local Similarity 40.0%; Pred. No. 18;
 Matches 20; Conservative 7; Mismatches 19; Indels 4; Gaps 2;
 QY 52 CASCRAPP--HSDFCLG--CAAAPAPPRLWPIILGALSILTEVLGLLSG 97
 Db 153 CAFVFAVPAIHMEFALGQYAAKSPFAFRIMPALGAVGWTICVGAIVG 202

RESULT 8
 G69099
 Probable pyruvate synthase (EC 1.2.7.1) gamma chain - *Methanobacterium thermoautotrophicum*
 C;Species: *Methanobacterium thermoautotrophicum*
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000
 C;Accession: G69099
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
 Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funct
 A;Reference number: A69000; MUID:98037514; PMID:9371463
 A;Accession: G69099
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-261 <MTH>
 A;Cross-references: GB:AE000929; GB:AE000666; NID:G2622853; PIDN:AA886210.1; PID:G262287
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH1740
 C;Superfamily: pyruvate synthase gamma chain
 C;Keywords: coenzyme A; oxidoreductase

Query Match 12.1%; Score 73.5; DB 2; Length 261;
 Best Local Similarity 29.2%; Pred. No. 8.8;
 Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;
 QY 31 PGTPAPCSGRSSWSA-----DLDKCMDASCRA-----RPHS---DFCLGCA-AAPPA 73
 Db 191 PGSTVKNKTSWRTFRKVLVDKDCIDCNCILCPGECINREHEIDYDYCKGCGICAEKC 250
 QY 74 PFRLL 78
 Db 251 PVKAI 255

RESULT 9
 T04420
 ribonuclease (EC 3.1.-.-) - barley
 C;Species: *Hordeum vulgare* (barley)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Jun-1999
 C;Accession: T04420
 R;Rogers, J.C.; Rogers, S.W.
 submitted to the EMBL Data Library, April 1997
 A;Reference number: Z15355
 A;Accession: T04420
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-227 <ROG>
 A;Cross-references: EMBL:AF000940; NID:G2150001; PIDN:AA858719.1; PID:G2150002
 A;Experimental source: cv. Igr1
 C;Genetics:
 A;Introns: 35/3; 87/3
 A;Superfamily: Enterobacter ribonuclease
 C;Keywords: hydrolase

Query Match 12.0%; Score 73; DB 2; Length 227;
 Best Local Similarity 30.0%; Pred. No. 8.8;
 Matches 30; Conservative 11; Mismatches 45; Indels 14; Gaps 4;
 QY 21 LLRSVAGEQAPGTAPCSRG--SSWSADLDKCMDCASCRARPHSDFCLGCAAPAPPAPRLIW 79
 Db 91 LLSSLRARWPTLACPASDGLQFWAHEWKHGTCAQMLFHEHYF---QTAAPRPAPLLD 147
 QY 80 PIL-----GGALSILTEVLGLL---SGFLVWRRCRRRS 109
 Db 148 ALASAGVADPGGYTYLSAVKGAIQQGTGFEPFVECNDES 187

RESULT 10
 D75303
 conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: D75303
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: D75303
 A;Status: preliminary

A:Molecule type: DNA
A:Residues: 1-346 <WHI>
A:Cross-references: GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF11754.1; PID:g646000
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2205
A:Map position: 1

Query Match 11.9%; Score 72.5; DB 2; Length 346;
Best Local Similarity 28.8%; Pred. No. 13;
Matches 32; Conservative 10; Mismatches 52; Indels 17; Gaps 5;

QY 12 LLVLGWLALLRSVAGEQAPGTAPCSRGSSWADLCKWDCASC---RAPHSD-----FC 64
DB 87 LVTCVGLGLV---TAGSASPTV-----MWGALVAFAVLATVWHLRPAAGSLFFVEA 138

QY 65 LGCAAA--PPAPFRLWPILGGLSLTFVLGLSLGFLVWRCHRRSSPPP 113
DB 139 VGTGALPHAPFLPALAVSGGAALSVLALGALCAWHSTRARPHELAAPPP 189

RESULT 11
A55624
fibrillin-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 02-Aug-2002
C:Accession: A55624
R:Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995
A:Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene
A:Reference number: A55624; MUID:95130561; PMID:7829516
A:Accession: A55624
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2871 <YIN>
A:Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
C:Genetics:
A:Gene: Fbn-1
C:Superfamily: fibrillin 1; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;
Best Local Similarity 25.3%; Pred. No. 75;
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

QY 36 CSRGSSWADLCKMD-----CASCARPHS-----DFCLGC 67
DB 2040 CPBGFSWSSGRRCQDLRWSYCAKFGGKSPKSRNHSKQCCCKALKGEGWGDPCCLC 2099

QY 68 AAAPPAPFRLWPILGAL 86
DB 2100 PTEPDFAFRQICPFGSGII 2118

RESULT 12
T36798
Probable transcription regulator soxR-like - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C:Accession: T36798
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
A:Reference number: Z21614
A:Accession: T36798
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-175 <OLI>
A:Cross-references: EMBL:AL095811; PIDN:CA846795.1; GSPDB:GN00070; SCOEDB:SCI30A.18c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCI30A.18c

Query Match 11.7%; Score 71; DB 2; Length 175;

Best Local Similarity 29.0%; Pred. No. 11;
Matches 29; Conservative 12; Mismatches 33; Indels 26; Gaps 5;

QY 2 ARGSRRLRLRLV---LGLWIALRSVAGEQAPGTAP-----CSRGSSWADLCKMDCA 53
DB 49 ARDALRRVAFVRAAQRVGIIPLATIREALAEPLPEGTFTEDDWARLSEWRSELDERIKOL 108

QY 54 SCRAPRHSDFCLGCAAPPPAPFRLWPILGGLSL--TFVL 92
DB 109 N-RLRDHLTDICG-----GCLSLSTCVL 131

RESULT 13
E95850
probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) ma
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: E95850
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: E95850
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC48469.1; PID:gl5139941; GSPDB:GN00167
R:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20069
A:Genome: plasmid
C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 11.6%; Score 70.5; DB 2; Length 467;
Best Local Similarity 26.4%; Pred. No. 26;
Matches 28; Conservative 14; Mismatches 21; Indels 43; Gaps 7;

QY 10 LRLVLGLWL-----ALLRSVAGEQA--PCTAPCSRGSS-----SWSADLD 47
DB 322 LAIMVSGVWASGETGAVLSAAFAALPG-----YGNVLVTISLALFAFTTILGWAYAE 376

QY 48 KCMDCASCARPHSDFCLGCAAPPPAPFRLWPILGGLSLTF 90
DB 377 KCM-----EYLIGTASA--IPRIWTVAVFGATLSLDF 409

RESULT 14
I56545
glypican precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 31-Jan-2000
C:Accession: I56545; JCI281; FC1132
R:Litwack, E.D.; Stipp, C.S.; Kumbasar, A.; Lander, A.D.
J. Neurosci. 14, 3713-3724, 1994
A:Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-an
A:Reference number: I56545; MUID:94267529; PMID:8207484
A:Accession: I56545
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-558 <RES>
A:Cross-references: GB:L34067; NID:g506416; PIDN:AAA41251.1; PID:g506417
R:Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.
Biochem. Biophys. Res. Commun. 188, 395-401, 1992
A:Title: Cloning of a major heparan sulfate proteoglycan from brain and identification a

```

Query Match      11.4%; Score 69.5; DB 2; Length 424;
Best Local Similarity 29.7%; Pred. No. 30;
Matches 30; Conservative 11; Mismatches 35; Indels 25; Gaps 4;

Qy    3 RGSRLRLRLVLGWLALLRVAGEQAPGTAPCSRGSGWSADLDKMDCASCA----- 57
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    2 RGTRILTLALLLG---AGINACRNREAOQTAPPAAAAAQQAAPRKAASASPAPTATE 58
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Qy    58 ----RPHSDFCLGCAAA-----PPAPFLLWPILGGALS L 88
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    59 PAVSPAADGCLPAPAPVTAQPRPEQP-----LSGRGL 92
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

```

Search completed: February 11, 2004, 10:39:54
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2004, 10:32:48 ; Search time 13 Seconds
(without alignments)
412.388 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 508

Sequence: 1 MARGSLRLLELLVLGLA.....LSGFLVWRRCRRSSPPX 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	93.9	129	1 FN14_HUMAN	Q9np84 homo sapien
2	445	73.2	129	1 FN14_MOUSE	Q9cr75 m tumor nec
3	87	14.3	184	1 TL3C_HUMAN	Q9erj3 homo sapien
4	78	12.8	448	1 FBL5_RAT	Q9wv88 rattus norv
5	77	12.7	448	1 FBL5_MOUSE	Q9wv88 mus musculu
6	76.5	12.6	245	1 FLIP_SALTY	P54700 salmonella
7	73.5	12.1	81	1 PORD_METH	P56815 methanobact
8	72	11.8	1278	1 NPCL1_HUMAN	O15118 homo sapien
9	72	11.8	2871	1 FBN1_MOUSE	Q61554 mus musculu
10	70	11.5	443	1 FBL4_MOUSE	Q9wv99 mus musculu
11	70	11.5	558	1 GPC1_RAT	P35053 rattus norv
12	69.5	11.4	495	1 MLP2_DROME	Q24400 drosophila
13	69	11.3	180	1 PTTG_HUMAN	P53801 homo sapien
14	69	11.3	314	1 Y127_HUMAN	O14140 homo sapien
15	69	11.3	324	1 TNR6_RAT	Q63199 rattus norv
16	68.5	11.3	205	1 GSC1_HUMAN	O15499 homo sapien
17	68.5	11.3	431	1 YG84_METH	Q27719 methanobact
18	67.5	11.1	368	1 GP62_HUMAN	Q9bzj7 homo sapien
19	67.5	11.1	1008	1 VGLM_UUK	P09613 vukunieni v
20	67.5	11.1	1013	1 EPAS5_CHICK	P54755 gallus gall
21	67	11.0	319	1 BST1_RAT	Q63072 rattus norv
22	67	11.0	386	1 HXAD_MOUSE	Q62424 mus musculu
23	67	11.0	1005	1 EPAS_MOUSE	P54757 rattus norv
24	67	11.0	2871	1 FBN1_PIG	Q9cv36 sus scrofa
25	66.5	10.9	443	1 FBL4_CRIGR	O50508 cricetus
26	66	10.9	394	1 V689_PSEAE	P42514 pseudomonas
27	66	10.9	992	1 POLS_RUBUM	P08563 rubella vir
28	66	10.9	1238	1 JAG2_HUMAN	Q9y219 homo sapien
29	66	10.9	2318	1 NTC3_MOUSE	Q61982 mus musculu
30	66	10.9	2319	1 NTC3_RAT	Q9r172 rattus norv
31	65.5	10.8	245	1 FLIP_ECOLI	P33133 escherichia
32	65.5	10.8	2321	1 NTC3_HUMAN	Q9um47 homo sapien
33	65	10.7	453	1 HRA3_HUMAN	P83110 homo sapien

RESULT 1

ID	FN14_HUMAN	STANDARD;	PRT;	129 AA.
AC	Q9NP84; Q9HCS0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member Fn14 precursor (Fibroblast growth factor-inducible immediate-early response protein 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).			
GN	TNFRSF12A OR FN14.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=20216634; PubMed=10751351;			
RA	Feng S.-L.Y., Guo Y., Factor V.M., Thorgerirsson S.S., Bell D.W., Testa J.R., Peifley K.A., Winkles J.A.			
RA	"The Fn14 immediate-early response gene is induced during liver regeneration and highly expressed in both human and murine hepatocellular carcinoma."			
RL	Am. J. Pathol. 156:1253-1261 (2000).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Tanaka S., Sugimachi K.J.			
RA	"Human homologue of Fn14."			
RL	Submitted (DBJ-1999) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Uterus;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuller G.D., Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RP	[4]			
RP	FUNCTION.			

O08644 mus musculu
P23470 homo sapien
Q03499 hepatitis e
O95407 homo sapien
Q95967 homo sapien
Q01279 mus musculu
P16283 mus musculu
P49862 homo sapien
O75880 homo sapien
P17129 canis famil
P71809 mycobacteri
P83105 homo sapien

ALIGNMENTS

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RX MEDLINE=21585797; PubMed=11728344;
RA Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;
RT "A novel TNF receptor family member binds TWEAK and is implicated in
RL angiogenesis.";
CC Immunity 15:837-846(2001).
CC
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in
CC some cell types. Promotes angiogenesis and the proliferation of
CC endothelial cells. May modulate cellular adhesion to matrix
CC proteins.
CC
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC TRAF3.
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NP84-1; Sequence=Displayed;
CC
CC Name=2;
CC IsoId=Q9NP84-2; Sequence=VSP_006519;
CC
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and
CC kidney. Intermediate expression in lung, skeletal muscle and
CC pancreas.
CC
CC -!- INDUCTION: By fibroblast growth factor 1 (FGF1) and phorbol ester.
CC
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC
CC EMBL; AF191148; AAF69108.1; -
CC EMBL; AB033480; BAA94792.1; -
CC EMBL; AB033481; BAB17850.1; -
CC EMBL; BC002718; AAH02718.1; -
CC Genbank; HGNC:18152; TNFRSF12A.
CC MIM; 605914; -
CC GO; GO:0006928; P:cell motility; TAS.
CC GO; GO:0007275; P:development; TAS.
CC InterPro; IPR001368; TNFR_c6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
CC PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
CC Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal;
KW Alternative splicing.
FT SIGNAL 1 27
FT CHAIN 28 129
FT DOMAIN 28 80 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSMEM 81 101 SUPERFAMILY MEMBER FN14.
FT DOMAIN 102 129 EXTRACELLULAR (POTENTIAL).
FT REPEAT 36 67 POTENTIAL.
FT DISULFID 36 49 CYTOPLASMIC (POTENTIAL).
FT VARSPIC 33 67 TNFR-CYS (ATYPICAL).
FT
FT Missing (in isoform 2).
FT /FTID=VSP_006519
SQ SEQUENCE 129 AA; 13911 MW; BF3DFB93C1E1C448 CRC64;
Query Match 93.9%; Score 571; DB 1; Length 129;
Best Local Similarity 94.7%; Pred. No. 7.3e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTCPSRGSSWSADLDKCMDCASCRAAPH 60
Dd 1 MARGSLRLRLVLGLWLLALLRSVAGEQAPGTCPSRGSSWSADLDKCMDCASCRAAPH 60
QY 61 SDFCLGCAAPAPPRLLWPILGGALSLTFVLGLSGFVLWRCRRSSPPPP 113
Dd 61 SDFCLGCAAPAPPRLLWPILGGALSLTFVLGLSGFVLWRCRRRKRFTTP 113
RESULT 2

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FN14 MOUSE
ID FN14 MOUSE STANDARD; PRT; 129 AA.
AC Q9C75; Q90ZM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member Fn14 precursor
DE (Fibroblast growth factor-inducible immediate-early response protein
DE 14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)
DE (Tweak-receptor) (TweakR).
GN TNFRSF12A OR FN14 OR FGPRP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=Fibroblast;
RX MEDLINE=20020297; PubMed=1051889;
RA Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,
RA Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Richards C.M., Winkles J.A.;
RA "The mitogen-inducible Fn14 gene encodes a type I transmembrane
RA protein that modulates fibroblast adhesion and migration.";
RL J. Biol. Chem. 274:33166-33176(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.W., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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DOMAIN	127	EGF-LIKE 2, CALCIUM-BINDING	(POTENTIAL)
FT	167	EGF-LIKE 2, CALCIUM-BINDING	(POTENTIAL)
DOMAIN	168	EGF-LIKE 3, CALCIUM-BINDING	(POTENTIAL)
FT	206	EGF-LIKE 3, CALCIUM-BINDING	(POTENTIAL)
DOMAIN	207	EGF-LIKE 4, CALCIUM-BINDING	(POTENTIAL)
FT	246	EGF-LIKE 4, CALCIUM-BINDING	(POTENTIAL)

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```

CC CC EMBL; AF112151; AAD41767.1; -.
DR DR HSSP; P00736; IAPQ.
DR DR MGD; MGI:1346091; Ebln5.
DR DR InterPro; IPR000152; Asx hydroxyl.
DR DR InterPro; IPR001881; EGF Ca.
DR DR InterPro; IPR006209; EGF-like.
DR DR Pfam; PF00008; EGF; 4.
DR DR SMART; SM00179; EGF CA; 4.
DR DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR DR PROSITE; PS01186; EGF_2; 4.
DR DR PROSITE; PS01187; EGF CA; 6.
KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
KW Glycoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 448 FIBULIN-5.
FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 288 333 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT SITE 54 56 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 131 144 BY SIMILARITY.
FT DISULFID 138 153 BY SIMILARITY.
FT DISULFID 155 166 BY SIMILARITY.
FT DISULFID 172 181 BY SIMILARITY.
FT DISULFID 177 190 BY SIMILARITY.
FT DISULFID 192 205 BY SIMILARITY.
FT DISULFID 211 221 BY SIMILARITY.
FT DISULFID 217 230 BY SIMILARITY.
FT DISULFID 232 245 BY SIMILARITY.
FT DISULFID 251 262 BY SIMILARITY.
FT DISULFID 258 271 BY SIMILARITY.
FT DISULFID 273 286 BY SIMILARITY.
FT DISULFID 292 305 BY SIMILARITY.
FT DISULFID 299 314 BY SIMILARITY.
FT DISULFID 320 332 BY SIMILARITY.
FT CARBOHYD 283 283 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 448 AA; 50193 MW; F15CC70CFFBDC97 CRC64;

Query Match 12.7%; Score 77; DB 1; Length 448;
Best Local Similarity 24.1%; Pred. No. 2.8;
Matches 26; Conservative 8; Mismatches 24; Indels 50; Gaps 5;

QY 6 LRLRLVLLGLWLLALLRSVAGEQAPGTA--PCSRGSSWSADLDKCMDCASCRRPHSDF 63
Db 4 LKRLIVTILAUML-----PHGNAQQCTNGFDLDRQSGQCCLDIDECRTIPEA-- 52

QY 64 CLG-----C-----AAAPPAP 74
Db 53 CRGDMCMVQNGGYLCIPRTNVPYRGVPSNPSYTSYSGPYPAAPVP 100

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RESULT 6

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ID FLIP SALTY STANDARD; PRT; 245 AA.
AC P54700;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellar biosynthetic protein flip precursor.
GN FLIP OR FLAR OR STM1979.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
CX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
RC STRAIN=LT2;

```

```

RX MEDLINE=97464436; PubMed=9324257;
RA Ohsishi K., Fan F., Schoenheits G.J., Kihara M., Macnab R.M.;
RT "The FlpO, FlpP, FlpQ, and FlpR proteins of Salmonella typhimurium:
putative components for flagellar assembly.";
RN J. Bacteriol. 179:6092-6099(1997).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
CC -!- FUNCTION: Plays a role in the flagellum-specific transport system
(BY similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- MISCELLANEOUS: For insertion of flpP into the membrane, cleavage
of the signal peptide is important kinetically but not absolutely
required.
CC -!- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
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CC -----
EMBL; L49021; AAB81319.1; -.
DR EMBL; AE008787; AAL20891.1; -.
DR PIR; S78698; S78698.
DR StyGene; SG10577; flpP.
DR InterPro; IPR005837; FlpP.
DR InterPro; IPR005838; TypeIII_P.
DR Pfam; PF00813; FlpP; 1.
DR PRINTS; PR01302; TYPE3IMPPTOT.
DR ProDom; PD002586; TypeIII_P; 1.
DR TIGRFAMS; TIGR01103; flpP; 1.
DR PROSITE; PS01060; FLIP_1; 1.
DR PROSITE; PS01061; FLIP_2; 1.
KW Flagella, Transmembrane; Inner membrane; Transport; Protein transport;
KW Signal; Complete proteome.
FT SIGNAL 1 21
FT CHAIN 22 245 FLAGELLAR BIOSYNTHETIC PROTEIN FLIP.
FT TRANSMEM 45 65 POTENTIAL.
FT TRANSMEM 88 108 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
SQ SEQUENCE 245 AA; 26787 MW; C9A4241F0653A4D4 CRC64;

Query Match 12.6%; Score 76.5; DB 1; Length 245;
Best Local Similarity 30.8%; Pred. No. 1.8;
Matches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 6;

QY 6 LRLRLVLLGLWLLALLRSVAGEQAPG--TAP-CSRGSWSADLDKCMDCASCRRAP-- 59
Db 1 MRLLFLSLAGLW--LFSPAAAQPLGLISQPLAGGQSQMSLSVQTLVFTITSITFLPAL 58

QY 60 --HSDP-----CLGCAAPPAPFLWILGALSLTFVL 92
Db 59 LMTSFTRIIVFGLRLNALGTPSAPPNQV-----LLGLALELTFEI 100

RESULT 7
PORD METH
ID PORD METH STANDARD; PRT; 81 AA.
AC P56815;
DT 30-MAY-2000 (Rel. 39, Created)

```

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Pyruvate synthase subunit porD (EC 1.2.7.1) (Pyruvate oxidoreductase
 delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).
 GN POR OR MTHL740.1
 GN Methanobacterium thermoautotrophicum.
 OS Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Fatwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
 CC CoA + CO(2) + reduced ferredoxin.
 CC -1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS.
 CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
 CC GAMMA CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
 CC -1- CAUTION: THERE SEEMS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER
 CC PORC AND PORF. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AE000929; AAB86210.1; ALT_INIT.
 DR HSP: P00195; 1CLF.
 DR InterPro; IPR001450; 4FeS_ferredoxin.
 DR Pfam; PF00037; fer4; 2.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
 KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S;
 KW Complete proteome.
 FT METAL 34 34 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 FT METAL 37 37 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 FT METAL 40 40 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 FT METAL 44 44 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 FT METAL 60 60 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 FT METAL 63 63 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 FT METAL 66 66 IRON-SULFUR 2 (4FE-4S) (POTENTIAL).
 FT METAL 70 70 IRON-SULFUR 1 (4FE-4S) (POTENTIAL).
 SQ SEQUENCE 81 AA; 9121 MW; 219A9CAE8A41604 CRC64;
 Query Match 12.1%; Score 73.5; DB 1; Length 81;
 Best Local similarity 29.2%; Pred. No. 1.3;
 Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;
 QY 31 PGTAPCRSGSSNSA-----DLDKWDCASCRA-----RHSS---DFCLGCA-AAPPA 73
 Db 11 PGSTVKNKGTGSRFTFPLVDKDKDCDCNCLIFCPGECINRHEIDYDKCGCGCAEKC 70
 QY 74 PFRLL 78
 Db 71 PVKAI 75
 RESULT 8
 NPCL_HUMAN
 ID NPCL_HUMAN STANDARD; PRT; 1278 AA.

AC O15118; Q9P130;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Niemann-Pick C1 protein precursor.
 GN NPC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS NPC1.
 RC MEDLINE=97362323; PubMed=9211849;
 RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D.,
 RA Cummings C., Gu J., Rosenfeld W.A., Pavan W.J., Ioannou Y.A.,
 RA Nagle J., Polymeropoulos M.H., Sturley S.D., Ioannou Y.A.,
 RA Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R.,
 RA Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y.,
 RA Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J.,
 RA Markie D., O'Neill R.R., van Diggelen O.P., Ellender M.,
 RA Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.;
 RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol
 RT homeostasis.";
 RL Science 277:228-231(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS.
 RC MEDLINE=99355599; PubMed=10425213;
 RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
 RA Carstea E.D.;
 RT "The genomic organization and polymorphism analysis of the human
 RT Niemann-Pick C1 gene.";
 RL Biochem. Biophys. Res. Commun. 261:493-498(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21623216; PubMed=11754101;
 RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,
 RA Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;
 RT "NPC1: Complete genomic sequence, mutation analysis, and
 RT characterization of haplotypes.";
 RL Hum. Mutat. 19:30-38(2002).
 RN [4]
 RP CHARACTERIZATION.
 RC MEDLINE=99128318; PubMed=9927649;
 RA Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S.,
 RA Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III,
 RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and
 RT lysosomal targeting in cholesterol mobilization.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
 RN [5]
 RP VARIANT NPD TRP-992.
 RC MEDLINE=98299797; PubMed=9634529;
 RA Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M.,
 RA Byers D.M., Dobson M.J., Neumann P.E.;
 RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a
 RT G3097-->T transversion in NPC1.";
 RL Am. J. Hum. Genet. 63:52-54(1998).
 RN [6]
 RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; TRP-992; ALA-1007;
 RP THR-1061 AND VAL-1213.
 RC MEDLINE=99452586; PubMed=10521290;
 RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C.,
 RA Neumann P.E.;
 RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich
 RT domain.";
 RL Am. J. Hum. Genet. 65:1252-1260(1999).
 RN [7]
 RP VARIANT NPC1 THR-1061.
 RC MEDLINE=99452593; PubMed=10521297;
 RA Millat G., Marçais C., Rafi M.A., Yamamoto T., Morris J.A.,
 RA Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;
 RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant
 RT allele in patients of Western European descent and correlates with a
 RT classic juvenile phenotype.";

Am. J. Hum. Genet. 65:1321-1329 (1999).

[8] VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.

Yamamoto T., Namba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H., Akaboshi S., Watanabe Y., Takehima T., Inui K., Okada S., Tanaka A., Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G., Ohno K.,

"NPC1 gene mutations in Japanese patients with Niemann-Pick disease type C";

Hum. Genet. 105:10-16 (1999).

[9] VARIANTS NPC1 GLN-958 AND ALA-1007.

Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F., Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K., "Niemann-Pick C variant detection by altered sphingolipid trafficking and correlation with mutations within a specific domain of NPC1";

Am. J. Hum. Genet. 68:1361-1372 (2001).

[10] VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.

MEDLINE=21313105; PubMed=11333381;

Millat G., Marcalis C., Tomasetto C., Chikh K., Fensom A.H., Harzer K., Wenger D.A., Ohno K., Vanier M.T.

"Niemann-Pick C1 disease: correlations between NPC1 mutations, levels of NPC1 protein, and phenotypes emphasize the functional significance of the putative sterol-sensing domain and of the cysteine-rich luminal loop";

Am. J. Hum. Genet. 68:1373-1385 (2001).

[11] VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.

MEDLINE=21372069; PubMed=11479732;

Ribeiro I., Marcão A., Amaral O., Sa Miranda M.C., Vanier M.T., Millat G.

"Niemann-Pick type C disease: NPC1 mutations associated with severe and mild cellular cholesterol trafficking alterations";

Hum. Genet. 109:24-32 (2001).

-!- FUNCTION: INVOLVED IN THE INTRACELLULAR TRAFFICKING OF CHOLESTEROL. MAY PLAY A ROLE IN VESICULAR TRAFFICKING IN GLIA, A PROCESS THAT MAY BE CRUCIAL FOR MAINTAINING THE STRUCTURAL AND FUNCTIONAL INTEGRITY OF NERVE TERMINALS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. FOUND IN LATE ENDOSOMES AND LYOSOMES.

-!- DOMAIN: A CYSTEINE-RICH N-TERMINAL DOMAIN AND A C-TERMINAL DOMAIN CONTAINING A DI-LEUCINE MOTIF NECESSARY FOR LYOSOMAL TARGETING ARE CRITICAL FOR MOBILIZATION OF CHOLESTEROL FROM LYOSOMES.

-!- PTM: GLYCOSYLATED.

-!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease type C1 (NPC1) [MIM:257220]; an autosomal recessive lipid storage disorder, which affects particularly the brain, liver and spleen, and which is characterized by lysosomal accumulation of low density lipoprotein derived cholesterol. Clinical features include variable hepatosplenomegaly and severe progressive neurological dysfunction such as ataxia, dystonia and dementia. The age of onset can vary from infancy to late adulthood.

-!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease type D (NPD) [MIM:257250]; also called Niemann-Pick disease without sphingomyelinase deficiency, or Nova Scotian type. Because of evidence from biochemical changes, lack of complementation, and linkage mapping to the same chromosome site, NPD and NPC1 are considered to be allelic disorders.

-!- SIMILARITY: BELONGS TO THE PATCHED FAMILY.

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EMBL; AF002020; AAB63982.1; -

EMBL; AF157379; AAD48006.1; -

DR EMBL; AF157365; AAD48006.1; JOINED.

DR EMBL; AF157366; AAD48006.1; JOINED.

DR EMBL; AF157367; AAD48006.1; JOINED.

DR EMBL; AF157368; AAD48006.1; JOINED.

DR EMBL; AF157369; AAD48006.1; JOINED.

DR EMBL; AF157370; AAD48006.1; JOINED.

DR EMBL; AF157371; AAD48006.1; JOINED.

DR EMBL; AF157372; AAD48006.1; JOINED.

DR EMBL; AF157373; AAD48006.1; JOINED.

DR EMBL; AF157374; AAD48006.1; JOINED.

DR EMBL; AF157375; AAD48006.1; JOINED.

DR EMBL; AF157376; AAD48006.1; JOINED.

DR EMBL; AF157377; AAD48006.1; JOINED.

DR EMBL; AF157378; AAD48006.1; JOINED.

DR EMBL; AF157379; AAD48006.1; JOINED.

DR EMBL; AF157380; AAD48006.1; JOINED.

DR EMBL; AF157381; AAD48006.1; JOINED.

DR EMBL; AF157382; AAD48006.1; JOINED.

DR EMBL; AF157383; AAD48006.1; JOINED.

DR EMBL; AF157384; AAD48006.1; JOINED.

DR EMBL; AF157385; AAD48006.1; JOINED.

DR EMBL; AF157386; AAD48006.1; JOINED.

DR EMBL; AF157387; AAD48006.1; JOINED.

DR EMBL; AF157388; AAD48006.1; JOINED.

DR EMBL; AF157389; AAD48006.1; JOINED.

DR EMBL; AF157390; AAD48006.1; JOINED.

DR EMBL; AF157391; AAD48006.1; JOINED.

DR EMBL; AF157392; AAD48006.1; JOINED.

DR EMBL; AF157393; AAD48006.1; JOINED.

DR EMBL; AF157394; AAD48006.1; JOINED.

DR EMBL; AF157395; AAD48006.1; JOINED.

DR EMBL; AF157396; AAD48006.1; JOINED.

DR EMBL; AF157397; AAD48006.1; JOINED.

DR EMBL; AF157398; AAD48006.1; JOINED.

DR EMBL; AF157399; AAD48006.1; JOINED.

DR EMBL; AF157400; AAD48006.1; JOINED.

DR EMBL; AF157401; AAD48006.1; JOINED.

DR EMBL; AF157402; AAD48006.1; JOINED.

DR EMBL; AF157403; AAD48006.1; JOINED.

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28-FEB-2003 (Rel. 41, Last annotation update)

DT Fibrillin 1 precursor.
DE FBN1 OR FBN-1.
DN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=95130561; PubMed=7829516;
RA Yin W., Germiller J., Sanguineti C., Smiley E., Pangilinan T.,
RA Pereira L., Ramirez F., Bonadio J.;
RT "Primary structure and developmental expression of Fbn-1, the mouse
RT fibrillin gene.";
RL J. Biol. Chem. 270:1798-1806(1995).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=CD-1; TISSUE=Kidney;
RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
CC -1- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
CC FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
CC MICROFIBRILS (BY SIMILARITY).
CC -1- SIMILARITY: Contains 47 EGF-like domains.
CC -1- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L29454; AAA56840.1; -;
DR EMBL; U22493; AAA64217.1; -;
DR FIR; A55624; A55624.
DR HSSP; P35555; 1APJ.
DR MGD; MGI:95489; Fbn1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00068; EGF; 46.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00179; EGF_CA; 42.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS01187; EGF_CA; 43.
DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
KW Repeat; Signal; Multigene family.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 2871 FIBRILLIN 1.
FT DOMAIN 81 112 EGF-LIKE 1.
FT DOMAIN 115 146 EGF-LIKE 2.
FT DOMAIN 147 178 EGF-LIKE 3.
FT DOMAIN 246 287 EGF-LIKE 4.
FT DOMAIN 288 329 EGF-LIKE 5, CALCIUM-BINDING.
FT DOMAIN 330 401 TGFBP 1.
FT DOMAIN 402 446 PRO-RICH.
FT DOMAIN 449 489 EGF-LIKE 6.
FT DOMAIN 490 529 EGF-LIKE 7, CALCIUM-BINDING.
FT DOMAIN 530 571 EGF-LIKE 8, CALCIUM-BINDING.
FT DOMAIN 572 612 EGF-LIKE 9, CALCIUM-BINDING.
FT DOMAIN 613 653 EGF-LIKE 10, CALCIUM-BINDING.
FT DOMAIN 656 721 TGFBP 2.
FT DOMAIN 723 764 EGF-LIKE 11, CALCIUM-BINDING.
FT DOMAIN 765 806 EGF-LIKE 12, CALCIUM-BINDING.
FT DOMAIN 807 846 EGF-LIKE 13, CALCIUM-BINDING.

FT DISULFID 776 790 BY SIMILARITY.
 FT DISULFID 792 805 BY SIMILARITY.
 FT DISULFID 811 821 BY SIMILARITY.
 FT DISULFID 816 830 BY SIMILARITY.
 FT DISULFID 832 845 BY SIMILARITY.
 FT DISULFID 914 926 BY SIMILARITY.
 FT DISULFID 921 935 BY SIMILARITY.
 FT DISULFID 937 950 BY SIMILARITY.
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 FT DISULFID 1166 1180 BY SIMILARITY.
 FT DISULFID 1182 1195 BY SIMILARITY.
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 FT DISULFID 1326 1339 BY SIMILARITY.
 FT DISULFID 1333 1348 BY SIMILARITY.
 FT DISULFID 1350 1361 BY SIMILARITY.
 FT DISULFID 1367 1380 BY SIMILARITY.
 FT DISULFID 1374 1389 BY SIMILARITY.
 FT DISULFID 1391 1402 BY SIMILARITY.
 FT DISULFID 1408 1420 BY SIMILARITY.
 FT DISULFID 1415 1429 BY SIMILARITY.
 FT DISULFID 1431 1444 BY SIMILARITY.
 FT DISULFID 1450 1461 BY SIMILARITY.
 FT DISULFID 1456 1470 BY SIMILARITY.
 FT DISULFID 1472 1485 BY SIMILARITY.
 FT DISULFID 1491 1502 BY SIMILARITY.
 FT DISULFID 1497 1511 BY SIMILARITY.
 FT DISULFID 1513 1526 BY SIMILARITY.
 FT DISULFID 1610 1622 BY SIMILARITY.
 FT DISULFID 1617 1631 BY SIMILARITY.
 FT DISULFID 1633 1646 BY SIMILARITY.
 FT DISULFID 1652 1663 BY SIMILARITY.
 FT DISULFID 1658 1672 BY SIMILARITY.
 FT DISULFID 1674 1687 BY SIMILARITY.
 Query Match 11.8%; Score 72; DB 1; Length 2871;
 Best Local Similarity 25.3%; Pred. No. 44;
 Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;
 QY 36 CSRGSSWSALDKWCD-----CASCRRPHS-----DFCLGC 67
 DB 2040 CPEGFSWSSRRQDLRMSYCAKFEKGKCSKPKSRNHSKQCCCKALKEGWDPCCLC 2099
 QY 68 AAAPPAPRLWLPILGAL 86
 DB 2100 PTEDEAFQICPPGSGII 2118
 RESULT 10
 ID_FBL4_MOUSE STANDARD; PRT; 443 AA.
 AC Q9WVJ9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
 DE (Fibulin-4) (FBL-4) (Mutant p53 binding protein 1).

GN EFEMP2 OR FBLN4 OR MBP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 EX MEDLINE=9308589; PubMed=10380882;
 RA Gallagher W.M., Argentin M., Sierra V., Bracco L., Debussche L.,
 RA Conseiller E.;
 RT "MBP1: a novel mutant p53-specific protein partner with oncogenic
 RT properties";
 RL Oncogene 18:3608-3616 (1999).
 CC -|- SUBUNIT: BINDS PREFERENTIALLY TO P53 MUTANTS.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: Belongs to the fibulin family.
 CC -|- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC -----
 DR EMBL; AF104223; AAD45219.1; -;
 DR HSSP; P00736; IAPQ.
 DR MGD; MGI:1891209; Efemp2.
 DR InterPro; IPR00152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF00008; EGF; 4.
 DR PRINTS; PR00907; THROMBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 DR Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 443
 FT DOMAIN 36 81
 FT DOMAIN 123 163
 FT DOMAIN 164 202
 FT DOMAIN 203 242
 FT DOMAIN 243 282
 FT DOMAIN 283 328
 FT DISULFID 127 140
 FT DISULFID 134 149
 FT DISULFID 151 162
 FT DISULFID 168 177
 FT DISULFID 173 186
 FT DISULFID 188 201
 FT DISULFID 207 217
 FT DISULFID 213 226
 FT DISULFID 228 241
 FT DISULFID 247 258
 FT DISULFID 254 267
 FT DISULFID 269 281
 FT DISULFID 287 300
 FT DISULFID 294 309
 FT DISULFID 315 327
 FT CARBOHYD 198 198
 FT CARBOHYD 394 394
 FT CARBOHYD 443 AA; 49425 MW; 4969C0328A23DD88 CRC64;
 SQ SEQUENCE
 Query Match 11.5%; Score 70; DB 1; Length 443;
 Best Local Similarity 27.3%; Pred. No. 13;
 Matches 24; Conservative 5; Mismatches 33; Indels 26; Gaps 3;

QY 13 LVGLGLWLLRSVAGEQAP-----GTAPCRSSGSSWSADLDKCMDCASCARPHS----- 61
 DB 12 LLLWAFLLLLGASPODPEDPSYTECTDGYEWDAHQHCRDYNVCLTIPEACKGMKC 71
 QY 62 -----DFCLGCAAA-----PPAP 74
 DB 72 INHYGYILCLPSRAAIVSIDLHGEPPPP 99

RESULT 11
 GPC1 RAT
 ID GPC1 RAT STANDARD; PRT; 558 AA.
 AC P35053;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glypican-1 precursor (HSPG M12).
 GN GPC1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.
 RC TISSUE=Brain;
 RX MEDLINE=93038690; PubMed=1417860;
 RA Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.;
 RT "Cloning of a major heparan sulfate proteoglycan from brain and
 RT identification as the rat form of glypican."
 RL Biochem. Biophys. Res. Commun. 188:395-401(1992).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.
 RC STRAIN=New England Deaconess Hospital;
 RX MEDLINE=94267529; PubMed=8207484;
 RA Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.;
 RT "Neuronal expression of glypican, a cell-surface
 RT glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan,
 RT in the adult rat nervous system."
 RL J. Neurosci. 14:3713-3724(1994).
 CC -1- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS HEPARAN SULFATE.
 CC MAY PLAY AN IMPORTANT ROLE IN THE TROPHIC AND INJURY RESPONSES OF
 CC NEURONS.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -1- PTM: THIS CELL-ASSOCIATED GLYPICAN IS FURTHER PROCESSED TO GIVE
 CC RISE TO A MEDIUM-RELEASED SPECIES.
 CC -1- SIMILARITY: Belongs to the glypican family.
 CC -----
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 CC -----
 DR EMBL; L02896; AAA86439.1;
 DR EMBL; L34067; AAA41251.1;
 DR PIR; I56545; I56545.
 DR InterPro; IPR001863; Glypican.
 DR Pfam; PF01153; Glypican; 1.
 DR PROSITE; PS01207; GLYPICAN; 1.
 KW Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor;
 KW Extracellular matrix.
 FT SIGNAL 1 23
 FT CHAIN 24 530 GLYPICAN-1.
 FT PROPEP 531 558 REMOVED IN MATURE FORM (POTENTIAL).
 FT LIPID 530 530 GPI-ANCHOR (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 O-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 55 55 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT CARBOHYD 486 486 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

FT CARBOHYD 488 488 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT CARBOHYD 490 490 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT CONFLICT 21 21 T -> A (IN REF. 2).
 FT CONFLICT 312 312 Y -> N (IN REF. 2).
 FT CONFLICT 362 362 A -> G (IN REF. 2).
 FT CONFLICT 437 437 I -> G (IN REF. 2).
 FT CONFLICT 443 443 E -> D (IN REF. 2; AA SEQUENCE).
 FT CONFLICT 515 515 I -> T (IN REF. 2).
 SQ SEQUENCE 558 AA; 61734 MW; E2878A854B9A1D7F CRC64;
 Query Match 11.5%; Score 70; DB 1; Length 558;
 Best Local Similarity 37.7%; Pred. No. 16;
 Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;
 QY 11 RLVLGLWLLA--LLRSVAGEQAPCTAPCRSSGSSWSADLDKCMDCASCAR-----ARPHSDFC 64
 DB 221 RSFVQGLGVASDVVRKVA--QVPLAPECSSRA-----VMKLVYCAHGRGVGARGPCPDYC 272
 QY 65 ----LGCAA 69
 DB 273 RNVKLGCLA 281

RESULT 12
 MLP2 DROME
 ID MLP2 DROME STANDARD; PRT; 495 AA.
 AC Q24400; Q9V162;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Muscle LIM protein MLP84B.
 GN LIM3 OR MLP84B OR CG10699.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96387325; PubMed=8794860;
 RA Stronach B.E., Siegrist S.E., Beckerle M.C.;
 RT "Two muscle-specific LIM proteins in Drosophila."
 RL J. Cell Biol. 134:1179-1195(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.;
 RT "Muscle LIM proteins associate with muscle sarcomeres and require
 RT dMFP2 for their expression during Drosophila myogenesis."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson D.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195 (2000)
CC -!- FUNCTION: PLAYS A ROLE IN CELL DIFFERENTIATION LATE IN MYOGENESIS.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSION IS RESTRICTED TO THE
CC SOMATIC, VISCERAL, AND PHARYNGEAL MUSCLES. WITHIN THE SOMATIC
CC MUSCULATURE, MLP48B IS LOCALIZED AT THE ENDS OF MUSCLE FIBERS AT
CC THE POINT OF ATTACHMENT TO THE EPIDERMIS. THERE IS NO EXPRESSION
CC IN CARDIAC MESODERM OR IN FAT BODY.
CC -!- DEVELOPMENTAL STAGE: EXPRESSION IS BIPHASIC, PEAKING LATE IN
CC EMBRYOGENESIS (16-24 H EMBRYOS) AND DURING THE LARVAL TO PUPAL
CC TRANSITION, WHEN THE MUSCULATURE IS DIFFERENTIATING. FOUND IN
CC DEVELOPING MUSCLES OF THE VISCERAL AND SOMATIC MESODERM SUBSEQUENT
CC TO THE FORMATION OF THE MUSCLE PRECURSOR CELLS. DECREASED LEVELS
CC ARE STILL DETECTABLE IN ADULTS.
CC -!- SIMILARITY: TO THE VERTEBRATE CYSTEINE-RICH PROTEINS.
CC -!- SIMILARITY: Contains 5 LIM zinc-binding domains.
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CC
CC EMBL: X91245; CAA62627.1; -;
CC EMBL: AF090832; AAC61591.1; -;
CC EMBL: AE003672; AAF54063.1; -;
CC HSP: P32965; 1CTL.
CC FlyBase: FBgn0014863; MLP84B.
CC InterPro: IPR001781; LIM.
CC Pfam: PF00412; LIM; 5.
CC ProDom: PD000094; LIM; 5.
CC SMART: SM00132; LIM; 5.
CC PROSITE: PS00478; LIM DOMAIN 1; 5.
CC PROSITE: PS50023; LIM DOMAIN 2; 5.
CC Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis;
CC Developmental protein; Differentiation.
CC FT DOMAIN 12 63
CC FT DOMAIN 65 80
CC FT DOMAIN 66 71
CC FT DOMAIN 120 172
CC FT DOMAIN 175 180
CC FT DOMAIN 178 189
CC FT DOMAIN 222 274
CC FT DOMAIN 276 291
CC FT DOMAIN 325 377
CC FT DOMAIN 379 390
CC FT DOMAIN 421 473
CC FT DOMAIN 475 490
CC SEQUENCE 495 AA; 53525 MW; 2E559B9178B540BE CRC64;

Query Match 11.4%; Score 69.5; DB 1; Length 495;
Best Local Similarity 28.0%; Pred. No. 16;
Matches 23; Conservative 7; Mismatches 37; Indels 15; Gaps 2;

QY 20 ALLRSVAGEAP-----GTAPCRGSGWSADLDKMDCAS-----CRAPHSDFC 64
Db 110 AIAAPEGEGPCPGGYVAAEQMLARGSRHKECFCKGCKKGLDSILCECPDKNIYC 169
QY 65 LGCAAAAPPAPFRLLPILGAL 86
Db 170 KGYAKKFGPKGYGQGQGGAL 191
RESULT 13
PTTG HUMAN
ID PTTG HUMAN STANDARD; PRT; 180 AA.
AC PS3801; Q9NS09;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pituitary tumor-transforming gene 1 protein-interacting protein
DE (Pituitary tumor-transforming gene 1 protein-interacting protein
DE binding factor) (PBF).
GN PTTGLIP OR C21ORF1 OR C21ORF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX 1
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=98234553; PubMed=9570958;
RA Yaspo M.-L., Aaltonen J., Horelli-Kuitunen N., Peltonen L.,
RA Lehrach H.;
RT "Cloning of a novel human putative type Ia integral membrane protein
RL mapping to 21q22.3";
RL Genomics 49:133-136 (1998).
RN [2]
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND INTERACTION WITH PTTGL.
RX MEDLINE=20317150; PubMed=10781616;
RA Chien W., Pei L.;
RT "A novel binding factor facilitates nuclear translocation and
RT transcriptional activation function of the pituitary
RT tumor-transforming gene product.";
RL J. Biol. Chem. 275:19422-19427 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20283799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharte M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon, Lung, Muscle, and Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May facilitate PTTG1 nuclear translocation.
 CC -!- SUBUNIT: Interacts with PTTG1.
 CC -!- SUBCELLULAR LOCATION: According to Ref.2, it is found in the
 CC cytoplasm and in the nucleus. According to Ref.1, it is a type I
 CC membrane protein.
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC
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 CC EMBL; Z50022; CRA90325.1; -;
 DR EMBL; AF149785; AAF73770.1; -;
 DR EMBL; AL163300; CAB90552.1; -;
 DR EMBL; BC000415; AAH00415.1; -;
 DR EMBL; BC012858; AAH12858.1; -;
 DR EMBL; BC019295; AAH19295.1; -;
 DR EMBL; BC020983; AAH20983.1; -;
 DR Genbank; HGNC:13524; PTTG1P.
 DR MIM; 603784; -;
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0006006; P:protein-nucleus import; IDA.
 DR InterPro; IPR003659; Plexin-like.
 DR SMART; SM00423; PSI; 1.
 DR Transmembrane; Nuclear protein.
 KW TRANSMEM 97 117 POTENTIAL.
 FT DOMAIN 116 121 POLY-CYS.
 FT CONFLICT 9 19 PTPVWRRLIG -> ARRTGGCASV (IN REF. 2).
 FT CONFLICT 108 114 TLLIGIA -> NPPPGHC (IN REF. 2).
 SQ SEQUENCE 180 AA; 20323 MW; FIE66014D49ECIDE CRC64;
 Query Match 11.3%; Score 69; DB 1; Length 180;
 Best Local Similarity 25.8%; Pred. No. 7;
 Matches 32; Conservative 19; Mismatches 43; Indels 30; Gaps 7;
 QY 10 LRLVLGLWLLRSVAGEQAGTAPCGSGSWADLDKMCASCRCARPHSPDFCLG--- 66
 Db 15 LRLGGALLLLLPVAAQAQPPGAA-CSQNTKTC--EECLKNVCLNCNTKACLDYPV 71
 QY 67 CAAAPAP-----FRLW-----PILGGALSFTVLGLSGFLVWRRCRRER 108
 Db 72 TSVLPFASLCKLSARWGVWVNFALITWVVG-----TLLIGI--AICCCCCRRKR 125
 QY 109 SSPP 112
 Db 126 SRXP 129
 RESULT 14
 ID Y127 HUMAN STANDARD; PRT; 314 AA.
 AC Q14140;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein KIAA0127.
 GN KIAA0127.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=96127530; PubMed=8590280;
 RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
 RT "Prediction of the coding sequences of unidentified human genes. IV.
 RT The coding sequences of 40 new genes (K1AA0121-K1AA0160) deduced by
 RT analysis of cDNA clones from human cell line KG-1.";
 RL DNA Res. 2:167-174(1995).
 CC
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)
 CC
 CC EMBL; D50917; BAA09476.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 314 AA; 33896 MW; E43107FC565AAC31 CRC64;
 Query Match 11.3%; Score 69; DB 1; Length 314;
 Best Local Similarity 34.0%; Pred. No. 12;
 Matches 18; Conservative 6; Mismatches 27; Indels 2; Gaps 1;
 QY 30 AGTAPCGSGSWADLDKMCASCRCARPHSPDFCLGCAAPAPFRLWLPIL 82
 Db 112 SPSSHPCDLGS--TTPLEACLTASLLEDDDDTFTCTSQAMQPTAPTKLSPPAL 162
 RESULT 15
 ID TNR6 RAT STANDARD; PRT; 324 AA.
 AC Q63139;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
 DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen
 DE (CD95)).
 GN TNFRSF6 OR PT1 OR FAS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94128114; PubMed=7507668;
 RA Kimura K., Yamamoto M., Wakatsuki T.;
 RT "A variant mRNA species encoding a truncated form of Fas antigen in
 RT the rat liver.";
 RL Biochem. Biophys. Res. Commun. 198:666-674(1994).
 CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both (By similarity).
 CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC
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Search completed: February 11, 2004, 10:38:33
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:35:58 ; Search time 34 Seconds
(without alignments)
865.235 Million cell updates/sec

Title: US-10-062-599-59
Perfect score: 608
Sequence: 1 MARGSLRLRLVGLWIA.....LSGFLVWRRCRRSSPPPX 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	14.3	333	4 Q9BZG3	Q9BZG3 homo sapien
2	87	14.3	426	4 Q9BZG2	Q9BZG2 homo sapien
3	83.5	13.7	610	10 Q943G8	Q943G8 oryza sativ
4	79	13.0	341	6 Q9N0B3	Q9N0B3 macaca fasc
5	78.5	12.9	332	10 Q42839	Q42839 hordeum vul
6	78.5	12.9	387	11 Q8VD70	Q8VD70 mus musculus
7	77.5	12.7	219	11 Q8EM15	Q8EM15 mus musculus
8	76.5	12.6	245	16 Q8Z5R3	Q8Z5R3 salmone
9	75.5	12.4	222	12 Q9QEE6	Q9QEE6 indian citr
10	75.5	12.4	449	16 Q53668	Q53668 mycobacteri
11	75.5	12.4	635	5 Q18288	Q18288 caenorhabdi
12	75	12.3	370	4 Q96KN9	Q96KN9 homo sapien
13	75	12.3	411	16 Q8CXG1	Q8CXG1 oceanobacil
14	74.5	12.3	519	16 Q9A9X4	Q9A9X4 caulobacter
15	74	12.2	548	11 Q8K406	Q8K406 mus musculus
16	74	12.2	768	5 P90890	P90890 caenorhabdi

ALIGNMENTS

RESULT 1

Q9BZG3 PRELIMINARY; PRT; 333 AA.

AC Q9BZG3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Acid phosphatase variant 3.
GN ACPT.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=21309073; PubMed=11414767;
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that is highly expressed in the testis."
RL Genomics 74:385-395(2001).
DR EMBL; AF321318; AAK09396.1; --
DR HSSP; P15309; 2HPA.

DR InterPro; IPR000560; HisAc phsphtse.

DR Pfam; PF00328; acid phosphat; 1

DR PROSITE; PS00616; HIS-ACID-PHOSPHAT-1; 1.

DR PROSITE; PS00778; HIS-ACID-PHOSPHAT-2; 1.

SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;

Query Match 14.3%; Score 87; DB 4; Length 333;

Best Local Similarity 35.3%; Pred. No. 0.45;

Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY 31 PG-TAPCSGSSNSADLDKMDKASCRAPHSDFCILGC--AAAPAPFRLMFLGALS 87

DB 258 PGCPAPCPGLRGFYQL-----TAPAPPAHGVSCHGPVEAIPAP---VVELLAGAVA 307

QY 88 LTFVLGLLSGLVWR--RCRRSSP 111

DB 308 VLVLSGLGLLAWRPGCLRALGGP 332

Q9P2P7 homo sapien
O04393 hordeum vul
Q9PQD6 xanthomonas
Q8NZR7 homo sapien
Q98TH8 cyprinus ca
Q96QA0 homo sapien
Q8NCO corynebacte
Q9QGD2 homo sapien
Q9RSC0 deinococcus
Q9Z288 homo sapien
Q9BZW8 homo sapien
Q9IAR7 gallus gall
Q818V6 giardia lam
Q95054 homo sapien
Q8W393 oryza sativ
Q93072 hepatitis g
Q90631 baboon herp
Q9S255 streptomyce
Q98J10 rhizobium l
Q9GF2 mus musculu
Q8ZP4 oryza sativ
Q9P3W7 xanthomonas
Q9FCA1 streptomyce
Q92X93 rhizobium m
Q961P0 homo sapien
Q75637 human immun
Q9PDE9 xanthomonas
Q9TT10 sus scrofa
Q9UJA2 homo sapien

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RESULT 2
Q9BZG2 ID Q9BZG2 PRELIMINARY; PRT; 426 AA.
AC Q9BZG2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Acid phosphatase.
GN ACPT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=21309073; PubMed=11414767;
RA Yusuf G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
is highly expressed in the testis.";
RL Genomics 74:385-395(2001).
DR EMBL; AF321918; AAK09393.1; -.
DR HSP; P15309; 2HPA.
DR Genew; HGNC:14376; ACPT.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; acid_phosphat_1; 1.
DR PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
DR PROSITE; PS00778; HIS ACID PHOSPHAT 2; 1.
SQ SEQUENCE 426 AA; 46089 MW; BE930398041DB061 CRC64;

Query Match 14.38; Score 87; DB 4; Length 426;
Best Local Similarity 35.38; Pred. No. 0.57;
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY 31 PG-TAPCSRGSSWSADLCKMDCASCRCARPHSDFCLGC--AAAPPAPFRLWLPILGALS 87
Db 351 PGCPACPLGRFYQL-----TAPAPPAHGVSCHGPEAALPPAP---VPLLAGAVA 400

QY 88 LTFVLGLSGFLVWR-RCRERSSP 111
Db 401 LVVALSLGLGLLAWRPGLRALGGP 425

RESULT 3
Q943G8 ID Q943G8 PRELIMINARY; PRT; 610 AA.
AC Q943G8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative receptor protein kinase.
GN P0046E05.12.
OS Erykatia (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0046E05.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AP003237; BAB67905.1; -.
DR Gramene; Q943G8; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002230; Ser_Thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferrase.
SQ SEQUENCE 610 AA; 64405 MW; 2A7B3EBB83FA9303 CRC64;

Query Match 13.7%; Score 83.5; DB 10; Length 610;
Best Local Similarity 24.6%; Pred. No. 1.8;
Matches 34; Conservative 12; Mismatches 35; Indels 57; Gaps 4;

QY 30 APGTAPCSRGSSWSADLCKMDC-----CASCRCARPHSDF 63
Db 84 SPGDSSTVGTGSSTATVTASTDADPNAGDAVPTSGAGDAIPSSACRKPAAACFNRPATD- 142
QY 64 CLGCAAPAPFPELLWP-----ILGALSITTFVLGLSG- 97
Db 143 --NVPASPPPPRISLSPPPPPTSGSGSSKSNNGTVAAGVAVVVGLAAGL 200
QY 98 --FLVWRRCRRERSPPPP 113
Db 201 IYFFVSKRRRRRQHPPPP 218

RESULT 4
Q9NOB3 ID Q9NOB3 PRELIMINARY; PRT; 341 AA.
AC Q9NOB3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Unnamed protein product (Gap junction protein) (Connexin).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL
(BY SIMILARITY).
CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.
DR EMBL; AB046017; BAB01599.1; -.
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS 1; 1.
DR PROSITE; PS00408; CONNEXINS 2; 1.
KW Gap junction; Transmembrane.
SQ SEQUENCE 341 AA; 36784 MW; 4A71DEA938F0FA0C CRC64;

Query Match 13.0%; Score 79; DB 6; Length 341;
Best Local Similarity 27.9%; Pred. No. 3.1;
Matches 29; Conservative 9; Mismatches 46; Indels 20; Gaps 1;

QY 9 LRLTLVGLLWLLRSLVAGEAPGTAPCSRGSSWSADLCKMDCASCRCARPHSDFCLGCA 68
Db 119 LRLTLEAFAFGALNYLLFGFLAPNKFCT-----RPPCTGVVDY 158
QY 69 AAPAPFPELLWPIILGALSITTFVLGLSGFLVWRRCRRERSPP 112
Db 159 VSRTEKSLMLFLWVAWSALSLGLGLADLVCLSLRLMLRRRPPPP 202

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RESULT 5
Q42839 ID Q42839 PRELIMINARY; PRT; 332 AA.
AC Q42839;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chitinase (EC 3.2.1.14).
GN CHI33.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=95078949; PubMed=7987416;
RA Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,
RA Mundy J.;
RT "Identification of an enhancer/silencer sequence directing the
RT aleurone-specific expression of a barley chitinase gene.";
RL Plant J. 6:579-589 (1994).
DR EMBL: L34211; AAA56787.1; -.
DR HSP; P23951; ZBA.
DR InterPro: IPR001002; Chitin binding 1.
DR InterPro: IPR000726; Glyco_hydro_19.
DR Pfam: PF00187; Chitin bind_1; 1.
DR Pfam: PF00182; Glyco_hydro_19; 1.
DR PRINTS: PR00451; CHITINBINDING.
DR ProDom: PD000609; Chitin binding_1; 1.
DR ProDom: PD000574; Glyco_hydro_19; 1.
DR SMART: SM00270; ChtBD1; 1.
DR SMART: SM00270; ChtBD1; 1.
DR PROSITE: PS00773; CHITINASE_19_1; 1.
DR PROSITE: PS00774; CHITINASE_19_2; 1.
DR PROSITE: PS00026; CHITIN_BINDING; 1.
DR Chitin-binding; Glycosidase; Hydrolase.
KW Chitin-binding; Glycosidase; Hydrolase.
SQ SEQUENCE 332 AA; 35369 MW; 1B38554F49AC9E0F CRC64;

Query Match 12.9%; Score 78.5; DB 10; Length 332;
Best Local Similarity 32.0%; Pred. No. 3.4;
Matches 33; Conservative 9; Mismatches 38; Indels 23; Gaps 7;

Qy 13 LVIGLWIALRSV-----AGEAQP-TAP-----CSRGSWSADLQKMDCAACRAPHSD 63
Db 13 IVLSAALAMVMVRAQCGSQAGGATCPNCLCSRFGYCGSTSDYC--GAGCQSQ----- 65

Qy 64 CLGCAAPAPFRLWPILGALSITFVLGSLGLVWR-RCR 105
Db 66 CSGCGTPPGSP-----GGVSSIIISRDLEQFLLRDRQC 102

RESULT 6
Q8VD70 ID Q8VD70 PRELIMINARY; PRT; 387 AA.
AC Q8VD70;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 12.
GN TNFRSF25 OR TNFRSF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Straussberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC017526; AAH17526.1; -.
DR MGD; MGI:1934667; Tnfrsf25.

Query Match 12.7%; Score 77.5; DB 11; Length 219;
Best Local Similarity 30.0%; Pred. No. 2.9;
Matches 30; Conservative 16; Mismatches 45; Indels 9; Gaps 4;

Qy 19 LALLRSVAGQAPGTAPCSRGSWS--SADLQKMDCAACRAPHSDFCGLCAAP-PAPF 75
Db 99 LAGLRQSLDKPCASPCNLNGGTCRVASGIFEC---TCSAGSFGQFCVVKTLPPLPF 154

Qy 76 RLWLPILGALS--LTFVLGSLGLVWRRCRRSSPPP 113
Db 155 PLLEVAVPAACACLLLLGLLGLSGLIARKRQSEGTYP 194

DR InterPro: IPR000488; Death.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001388; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;

Query Match 12.9%; Score 78.5; DB 11; Length 387;
Best Local Similarity 18.9%; Pred. No. 3.9;
Matches 35; Conservative 21; Mismatches 44; Indels 85; Gaps 7;

Qy 4 GSRLRLRLVIGLWIALRSVAGE-----QA 30
Db 18 GSTARVLQPLFLPLLLLLLLLLGGQGGMGRCDCASESQRYGPFCCRCGPKGHYMK 77
Qy 31 PGTAPC-----SRGSWSADLQKMDC-----ASCRARP-----HS 61
Db 78 PCAEPCGNSTCLPCPSDTFLRDNHFKTDCTCCQVCDEALQVTLNCSAKSDTHCGQS 137
Qy 62 DFCIGCAAP-----PAPFRLWPILGALSITFVLG--LLSGFLV 100
Db 138 GWCVDCTEPCGKSPFCGATTPVHEAPTLEW--VQVLLGVAFGLGALICAYCR 195
Qy 101 WRRCR 105
Db 196 WQPCX 200

RESULT 7
Q8BMT5 ID Q8BMT5 PRELIMINARY; PRT; 219 AA.
AC Q8BMT5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE weakly similar to neurogenic locus notch 3 protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Porelimb;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL: AK031068; BAC27237.1; -.
DR NON_TER
FT
SQ SEQUENCE 219 AA; 23098 MW; 9F2C4BE237F9B522 CRC64;

Query Match 12.7%; Score 77.5; DB 11; Length 219;
Best Local Similarity 30.0%; Pred. No. 2.9;
Matches 30; Conservative 16; Mismatches 45; Indels 9; Gaps 4;

Qy 19 LALLRSVAGQAPGTAPCSRGSWS--SADLQKMDCAACRAPHSDFCGLCAAP-PAPF 75
Db 99 LAGLRQSLDKPCASPCNLNGGTCRVASGIFEC---TCSAGSFGQFCVVKTLPPLPF 154

Qy 76 RLWLPILGALS--LTFVLGSLGLVWRRCRRSSPPP 113
Db 155 PLLEVAVPAACACLLLLGLLGLSGLIARKRQSEGTYP 194
```


RESULT	8
ID	Q825R3
ID	Q825R3 PRELIMINARY; PRT; 245 AA.
AC	Q825R3;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Flagellar biosynthetic protein FlpP.
GN	SYZ187.
OS	Salmonella typhi.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;	
ON	[1]
OR	SEQUENCE FROM N.A.
RP	STRAIN=CT18;
RC	MEDLINE=21534947; PubMed=11677608;
RX	Parikh J., Dungan G., James K.D., Thomson N.R., Pickard D., Wain
RA	Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia N.
RA	Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA	Cronin A., Davis P., Davies R.M., Dowd L., White N., Parrar J.,
RA	Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA	Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Barry C.,
RA	Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA	Whitehead S., Barrell B.G.;
RT	"Complete genome sequence of a multiple drug resistant Salmonella
RT	enterica serovar Typhi CT18.";
RL	Nature 413:848-852(2001).
DR	EMBL; AL627272; CAD05727.1; -
DR	InterPro; IPR005837; FlpP.
DR	InterPro; IPR005838; TypeIII_P.
DR	Pfam; PF00813; FlpP; 1.
DR	PRINTS; PR01302; TYPE3IMPPROT.
DR	ProDom; PD002586; TypeIII_P; 1.
DR	TIGRFAMs; TIGR01103; flpP; 1.
DR	PROSITE; PS01060; FLIP_1; 1.
DR	PROSITE; PS01061; FLIP_2; 1.
KW	Complete proteome.
QY	SEQUENCE 245 AA; 26755 MW; C9B9931F0653A4D4 CRC64;
QY	Query Match 12.6%; Score 76.5; DB 16; Length 245;
QY	Best Local Similarity 30.8%; Pred.No. 4.1; Mismatches 33; Conservative 9; Mismatches 38; Indels 27; Gaps 1
DB	1 MERLLFLSLAGLW--LFSFAAAQLPGLISQPLAGGQGSWSLSVQTLVFTLSLTFLE
QY	60 ---HSDF-----CLGCAAAPAPFRLWPLTGLGALSILFVL 92
DB	59 LMTVSFRIIIVFGLLRNALGTSPAPNQV-----LLGLAFLTFPI 100
QY	Q9QEE6 PRELIMINARY; PRT; 222 AA.
ID	Q9QEE6
AC	Q9QEE6;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	23kDa protein (Putative 23 kDa nucleic acid binding protein).
DE	Indian citrus ringspot virus
OC	Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=104664;	
ON	[1]
OR	SEQUENCE FROM N.A.
RP	STRAIN=K1;
RX	MEDLINE=20496665; PubMed=11043349;
RA	Rustici G., Accotto G.P., Noris E., Masenga V., Luisoni E.,
RA	Milne R.G.;
RA	"Indian citrus ringspot virus: a proposed new species with some
RT	affinities to potex-, carla-, fovea- and allxiviruses.";
RT	Arch. Virol. 145:1895-1908(2000).

[2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=KL;
 RC
 RA Rustici G., Milne R.G., Accotto G.P.;
 RT "Nucleotide sequence, genome organization and phylogenetical analysis
 of Indian citrus ringpot virus.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF184962; AAF01314.1; -
 DR ENBL: AF406744; AAK97527.1; -
 SQ SEQUENCE 222 AA; 25455 MW; 636A47058DD8D01D CRC64;
 Query Match 12.4%; Score 75.5; DB 12; Length 222;
 Best Local Similarity 35.4%; Pred. No. 4.7;
 Matches 35; Conservative 7; Mismatches 38; Indels 19; Gaps
 QY 3 RGSRLRLLLVLGLWLLALRSVAGEQAP-CTAPCSRGSSWSADLKDMDCASRA--RP 59
 Db 21 RGSQIRSVLLP---WRPRTFPV---CPSPGSPYSRGTHSQPSYVRQNCERARQWFA 74
 QY 60 H-SDFCL-----GCAAAPAPPAPFRLL---WPILGALS 88
 Db 75 HDGPRCLHQRPYSRLQAPDPDPFHLSNFEPIALLAALSV 113
 RESULT 10
 O53668 PRELIMINARY; PRT; 449 AA.
 AC
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative membrane protein.
 GN RV0246 OR MT0260 OR MTV034.12.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=H37Rv;
 RC
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RL Nature 393:537-544(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CDC 1551 / Oshkosh;
 RC Fletschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Karonay J.F., Nelson W.C., Umayar L.A., Ermolaeva M., Salzberg S.L.,
 RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL021929; CAA17338.1; ALT_INIT.
 DR ENBL: AB006934; AAK44478.1; -
 DR TIGR: MT0260; -
 DR Tuberculelist; RV0246; -
 KW Complete proteome.
 SQ SEQUENCE 449 AA; 46926 MW; FCE6EF930F03D1E6 CRC64;
 Query Match 12.4%; Score 75.5; DB 16; Length 449;
 Best Local Similarity 23.0%; Pred. No. 9.2;
 Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps

QY 1 MARGSLRLRLRLVGLMLALLRSVAGQA--PGTAPCSRGSS--WSADLDKMDCASCR 56
 DB 155 MPSTGATARILLTEVGVGAALTAVVAATLSFVDPQHPLSRNLHLWTAANVAISAAICR 214
 QY 57 ARHSDFCLGCAAPPAFRLLM-----PIIGG----- 84
 DB 215 ALPHR--IVPRVHAAPGLHKLIVGVGTAIRNGWYRRLVQLVGVSVLGSSFSHSIRVA 272
 QY 85 -----ALSLTFVLGLLGSFLVWRRCR 105
 DB 273 AVPGQPDPVAVVLFVCGVGLLGGIALNRYR 304
 RESULT 11
 ID O18288 PRELIMINARY; PRT; 635 AA.
 AC O18288;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ZK1010.9 protein.
 GN ZK1010.9
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
 OC Rhabditiidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gardner A., Mcmurray A.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81503; CAB04115.1; -.
 DR EMBL; Z82083; CAB04115.1; JOINED.
 DR EMBL; Z82083; CAB04975.1; -.
 DR EMBL; Z81503; CAB04975.1; JOINED.
 DR WormPep; ZK1010.9; CE23490.
 DR InterPro; IPR000175; Na/ntran_sympot.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_sympot; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 635 AA; 71267 MW; 2841834039D8F14A CRC64;
 Query Match 12.4%; Score 75.5; DB 5; Length 635;
 Best Local Similarity 36.6%; Pred. No. 13;
 Matches 26; Conservative 10; Mismatches 28; Indels 7; Gaps 3;
 QY 31 PGTAPCSRGSSWSADLDKMDCASCRARP--HSDFCLG--CAAAPPAPFRLLWILGGAL 86
 DB 92 PTTAYKNGGLSF---LIAYVVGILFAVPAIHMBFALGQYAAKSPPAAFREMMPILEGVG 148
 QY 87 SLTFVLGLLGS 97
 DB 149 WMTCLVGAIG 159
 RESULT 12
 ID O96KN9 PRELIMINARY; PRT; 370 AA.
 AC O96KN9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Connexin40.1 (Gap junction protein).
 GN CX40.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eiberger J., Soehl G., Willecke K.;

RT "Structural and functional diversity of connexin genes in the mouse
 and human genome.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
 CC PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
 CC MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.
 DR EMBL; AJ414564; CAC93846.1; -.
 DR InterPro; IPR000500; Connexin.
 DR Pfam; PF00029; connexin; 1.
 DR PRINTS; PR00206; CONNEXIN.
 DR SMART; SM00037; CNX; 1.
 DR PROSITE; PS00407; CONNEXINS_1; 1.
 DR PROSITE; PS00408; CONNEXINS_2; 1.
 KW Gap junction; Transmembrane.
 SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;
 Query Match 12.3%; Score 75; DB 4; Length 370;
 Best Local Similarity 27.9%; Pred. No. 8.6;
 Matches 29; Conservative 9; Mismatches 46; Indels 20; Gaps 1;
 QY 9 LLRLVGLMLALLRSVAGQAQGTAPCSRGSSWSADLDKMDCASCRARPHSDFCLGCA 68
 DB 148 LLRTLLEAAGALHYFLFGFLAPKKFCT-----RPPCTGWVDCY 187
 QY 69 AAPAPFRLLWILGGALSLTFVLGLLGSFLVWRRCRSSPP 112
 DB 188 VSRPTEKSLMLFLWAVSALSFLGLADLVCSLRRMRRRGPP 231
 RESULT 13
 ID O8CXG1 PRELIMINARY; PRT; 411 AA.
 AC O8CXG1;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Multidrug resistance protein (Efflux transporter).
 GN OBI706.
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
 OX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments.";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 DR EMBL; AP004598; BAC13662.1; -.
 KW Complete proteome.
 SQ SEQUENCE 411 AA; 45188 MW; 589B48F6EC39275A CRC64;
 Query Match 12.3%; Score 75; DB 16; Length 411;
 Best Local Similarity 27.6%; Pred. No. 9.5;
 Matches 32; Conservative 13; Mismatches 33; Indels 38; Gaps 5;
 QY 17 LWLALLRSVAGQAQGTAPCS-----RGSSWSADLDKMDCASCRARPHSDFCLGCA 68
 DB 102 IWLIIIGIIGIAGCTFTIAMALIGDLFGSSQSK-----MLGIY 142
 QY 69 AAPAPFRLLWILGGALSL-----TF-VLGLLGSFLV--WRRCRSSPPPP 113
 DB 143 EAGNELGKVLSPIIGAFAFALITWVFVFTFVISFLCALVFFVFFIKERRNRQTPTP 198
 RESULT 14

Q9A9X4
ID Q9A9X4 PRELIMINARY; PRT; 519 AA.
AC Q9A9X4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein CC0837.
GN CC0837.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Winn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of *Caulobacter crescentus*.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
DR EMBL; AB005760; AAK22822.1; -;
DR TIGR; CC0837; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 519 AA; 53934 MW; F37A3A52753DB53B CRC64;

Query Match 12.3%; Score 74.5; DB 16; Length 519;
Best Local Similarity 24.3%; Pred. No. 13;
Matches 33; Conservative 21; Mismatches 51; Indels 31; Gaps 4;

QY 9 LRLVLGLMLALLRS-VAGEQAPGTAPCSRGSS-----SWSADLDKCMD 51
DB 250 LLILMGLGLFLFAQVLGKRFADAAAGTGAETRAAKGPFVGAFAAGFQATLRKELR 309

QY 52 CASCRAPHSDFCLGCAAPAPPRLL-----WPILGALSILFVLGLSLGFLVWRR 103
DB 310 LVSRDAALLSQVLRVLVYVPIAFVWVRGAESLPWALAGFAAAVTFLAGVAGSLIWI 369

QY 104 CRRERS-----SPPP 113
DB 370 VSAEDTPDLAISPTP 385

RESULT 15
Q8K406 PRELIMINARY; PRT; 548 AA.
AC Q8K406
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leubrin/leucine-rich glioma inactivated 1-like protein (Weakly similar
DE to leucine-rich glioma-INACTIVATED 1 protein).
GN LGI3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Yun H.-Y., Lee S.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AF515590; AAM55219.1; -;
DR EMBL; AK049831; BAC33943.1; -;
DR MGD; MGI:2182619; Igi3.
DR InterPro; IPR005492; EFTP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF03736; EFTP; 2.
DR Pfam; PF00560; LRR; 1.
DR Pfam; PF01463; LRRCT; 1.
DR SMART; SM00369; LRR_Typ; 3.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS00506; LRR_TYPICAL; 1.
SQ SEQUENCE 548 AA; 61817 MW; 2DB303936354B958 CRC64;

Query Match 12.2%; Score 74; DB 11; Length 548;
Best Local Similarity 40.4%; Pred. No. 16;
Matches 21; Conservative 5; Mismatches 24; Indels 2; Gaps 1;

QY 3 RGSIRRLRLRLVGLMLALLRSVAGEQAPGTAPCSRGSSWSADLDKMDCAS 54
DB 8 RGFGRLLVLTGLGFCMLL--QVSARPPKTPPCPPSCSCTRTDTAFCDVSKS 57

Search completed: February 11, 2004, 10:39:21
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:37:18 ; Search time 21 Seconds
(without alignments)
229.688 Million cell updates/sec

Title: US-10-062-599-59
Perfect score: 608
Sequence: 1 MARGSLRRLLRLVGLWLA.....LSGFLVRRCRERSPPPX 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	99.8	114	4	US-09-690-454-59
2	274.5	45.1	112	4	US-09-489-847-139
3	274.5	45.1	155	4	US-09-489-847-284
4	274.5	45.1	156	4	US-09-489-847-228
5	96.5	15.9	248	4	US-09-252-991A-29249
6	88.5	14.6	400	4	US-09-252-991A-26145
7	87.5	14.4	631	4	US-09-252-991A-20063
8	83.5	13.7	152	4	US-09-252-991A-31619
9	80.5	13.2	249	4	US-09-252-991A-29850
10	76.5	12.6	250	4	US-09-322-409-31
11	76.5	12.6	250	4	US-09-451-527-31
12	76.5	12.6	276	4	US-09-322-409-26
13	76.5	12.6	276	4	US-09-451-527-26
14	75	12.3	334	4	US-09-252-991A-18795
15	74.5	12.3	305	4	US-09-252-991A-21147
16	73.5	12.1	187	4	US-09-199-637A-287
17	73.5	12.1	187	4	US-09-252-991A-21454
18	72	11.8	1278	4	US-09-462-136-2
19	72	11.8	3724	2	US-08-804-227C-10
20	72	11.8	3724	2	US-08-804-198-4
21	71.5	11.8	478	4	US-09-252-991A-22078
22	70.5	11.6	402	4	US-09-252-991A-18195
23	70	11.5	720	4	US-09-996-243-231
24	69.5	11.4	176	4	US-09-252-991A-25290
25	69	11.3	152	4	US-09-252-991A-24730
26	69	11.3	153	4	US-09-252-991A-20688
27	69	11.3	215	3	US-09-220-528-104

28	69	11.3	511	4	US-09-252-991A-28223	Sequence 28223, A
29	68.5	11.3	205	2	US-08-775-009-37	Sequence 37, Appl
30	68.5	11.3	429	1	US-07-964-589-2	Sequence 2, Appl
31	68.5	11.3	429	5	PCT-US93-02024-2	Sequence 2, Appl
32	68	11.2	139	4	US-09-252-991A-17414	Sequence 17414, A
33	68	11.2	144	4	US-09-252-991A-17313	Sequence 17313, A
34	68	11.2	204	4	US-09-252-991A-29996	Sequence 29996, A
35	68	11.2	282	4	US-09-252-991A-29124	Sequence 29124, A
36	68	11.2	365	4	US-09-252-991A-31958	Sequence 31958, A
37	68	11.2	775	4	US-09-252-991A-22300	Sequence 22300, A
38	67.5	11.1	174	3	US-09-383-586-12	Sequence 12, Appl
39	67.5	11.1	268	4	US-09-322-409-23	Sequence 23, Appl
40	67.5	11.1	268	4	US-09-451-527-23	Sequence 23, Appl
41	67.5	11.1	294	4	US-09-322-409-7	Sequence 7, Appl
42	67.5	11.1	294	4	US-09-451-527-7	Sequence 7, Appl
43	67.5	11.1	359	3	US-09-413-814-90	Sequence 90, Appl
44	67.5	11.1	361	3	US-09-413-814-77	Sequence 77, Appl
45	67	11.0	112	4	US-09-252-991A-21707	Sequence 21707, A

ALIGNMENTS

RESULT 1
US-09-690-454-59
; Sequence 59, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-09-690-454-59

Query Match 99.8%; Score 607; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-59;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARGSLRRLLRLVGLWLA...PCTAPCRGSSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRRLLRLVGLWLA...PCTAPCRGSSWSADLDKCMDCASCARPH 60

Qy	61	SDFCLGCAAPPAPFRLIWPILGGALSTFVLGLSGFLVWRCRRERSPPP	113
Db	61	SDFCLGCAAPPAPFRLIWPILGGALSTFVLGLSGFLVWRCRRERSPPP	113

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RESULT 2
US-09-489-847-139
; Sequence 139, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ03IP1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-139

```

```

Query Match      45.1%; Score 274.5; DB 4; Length 112;
Best Local Similarity 96.4%; Pred. No. 9e-23;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MARGSLRLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSGWSADLQKMDCA-SC 55
      |||||
Db 1 MARGSLRLRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSGWSADLQKMDCSFSC 56
      |||||

```

```

RESULT 3
US-09-489-847-284
; Sequence 284, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,557
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-284

```

```

Query Match      45.1%; Score 274.5; DB 4; Length 155;
Best Local Similarity 96.4%; Pred. No. 1.3e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps
0

QY 1 MARGSLRELLLVGLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKMCDA-SC 55
      |||||
Db 1 MARGSLRELLLVGLVGLWALLRSVAGEQAPGTAPCSRGSWSADLDKMCDCSTC 56
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```

```

RESULT 4
US-09-489-847-228
  Sequence 228, Application US/09489847
  Patent No. 6476195
  GENERAL INFORMATION:
  APPLICANT: Rosen et al
  TITLE OF INVENTION: 98 Human Secreted Proteins
  FILE REFERENCE: P2031Pl
  CURRENT APPLICATION NUMBER: US/09/489,847
  CURRENT FILING DATE: 2000-01-24
  EARLIER APPLICATION NUMBER: PCT/US99/17130
  EARLIER FILING DATE: 1998-07-29
  EARLIER APPLICATION NUMBER: 60/094,657
  EARLIER FILING DATE: 1998-07-30
  EARLIER APPLICATION NUMBER: 60/095,486
  EARLIER FILING DATE: 1998-08-05
  EARLIER APPLICATION NUMBER: 60/096,319
  EARLIER FILING DATE: 1998-08-12
  EARLIER APPLICATION NUMBER: 60/095,454
  EARLIER FILING DATE: 1998-08-06
  EARLIER APPLICATION NUMBER: 60/095,455
  EARLIER FILING DATE: 1998-08-06
  NUMBER OF SEQ ID NOS: 376
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 228
  LENGTH: 156
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: SITE
  LOCATION: (156)
  OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-228

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```

Query Match          45.1%; Score 274.5; DB 4; Length 156;
Best Local Similarity 96.4%; Pred. No. 1.3e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      1  MARGSLRRLLRLVLGLWLLALLRSVAGEAQTGAPCRSGSSWSADLDKCMDC A-SC 55
      |||
DB      1  MARGSLRRLLRLVLGLWLLALLRSVAGEAQTGAPCRSGSSWSADLDKCMDCSTSC 56
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RESULT 5
US-09-252-991A-29249
; Sequence 29249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196, 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29249
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

```

```

RESULT 5
US-09-252-991A-29249
, Sequence 29249, Application US/09252991A
, Patent No. 6551795
, GENERAL INFORMATION:
, APPLICANT: Marc J. Rubenfield et al.
, TITLE OF INVENTION: NUCLEIC ACID AND ADIN
, TITLE OF INVENTION: AERUGINOSA FOR DIAGN
, FILE REFERENCE: 107196.136
, CURRENT APPLICATION NUMBER: US/09/252,991A
, CURRENT FILING DATE: 1999-02-18
, PRIOR APPLICATION NUMBER: US 60/074,788
, PRIOR FILING DATE: 1998-02-18
, PRIOR APPLICATION NUMBER: US 60/094,190
, PRIOR FILING DATE: 1998-07-27
, NUMBER OF SEQ ID NOS: 33142
, SEQ ID NO 29249
, LENGTH: 248
, TYPE: PR
, ORGANISM: Pseudomonas aeruginosa

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US-09-252-991A-29249

Query Match 15.9%; Score 96.5; DB 4; Length 248;
Best Local Similarity 30.0%; Pred. No. 0.0062;
Matches 27; Conservative 9; Mismatches 23; Indels 31; Gaps 4;
QY 18 WLALLRSVAGE-----QAGTAPCSRG-----SWSADLDKCM 50
DB 38 WCSSRSGGAACRCCRASSTAPCSAPSATAAPRTGTSNCWAGAAPTCWSATTSRCR 97
QY 51 DCASCRARPHSD-FCIGCA---AAPAPER 76
DB 98 GCASSRRRTGRCWCAACSAPVASPPAAWK 127

RESULT 6

US-09-252-991A-26145
; Sequence 26145, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26145
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26145

Query Match 14.6%; Score 88.5; DB 4; Length 400;
Best Local Similarity 38.3%; Pred. No. 0.08;
Matches 23; Conservative 4; Mismatches 30; Indels 3; Gaps 2;
QY 18 WLALLRSVAGEQAGTAPCS--RGSSWSADLDKCMDCASCRARPHSDFCIGCA-AAPAP 74
DB 45 WSTARREFAPTAAGWRCAPWMAASNTATLSPRTSTASCRMPHRCSCACCAKSRPPAP 104

RESULT 7

US-09-252-991A-20063
; Sequence 20063, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20063
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20063

Query Match 14.4%; Score 87.5; DB 4; Length 631;
Best Local Similarity 32.6%; Pred. No. 0.17;
Matches 30; Conservative 6; Mismatches 43; Indels 13; Gaps 4;
QY 23 RSVAGEQAGTAPCSRG-SWS-ADLDKCM--DCASCRARPHSDFCIGCAAPAPRLL 78

DB 112 RSSRKSRYPPAWPCVGRSSRDWQCAWRACCRGSCATCSATP-----AATPSAAACC 162
QY 79 WFLIGGALSFLVGLLGLSGFLVWRRCRRSS 110
DB 163 WGRAGVAARYAWRCGTLAGASPTTSCRRSSSS 194

RESULT 8

US-09-252-991A-31619
; Sequence 31619, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31619
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31619

Query Match 13.7%; Score 83.5; DB 4; Length 152;
Best Local Similarity 29.7%; Pred. No. 0.092;
Matches 30; Conservative 7; Mismatches 37; Indels 27; Gaps 5;
QY 23 RSVAGEQAGTAPCSRGSSWSADLDKCMDC-----ASC--RARPHSDFCIGCAAPAP 74
DB 63 RTTNSASRPTPARCSRHAPGWLGSTRCACCGAAAGASCASATPTT-----TAAPPS 117
QY 75 FRLWPLIGGALSITFVLGLSGFLVWRRCRE---RSSPP 112
DB 118 APATWSASGRCAGN-----WRCNRAWGRCQSP 147

RESULT 9

US-09-252-991A-29850
; Sequence 29850, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29850
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29850

Query Match 13.2%; Score 80.5; DB 4; Length 249;
Best Local Similarity 30.5%; Pred. No. 0.35;
Matches 40; Conservative 8; Mismatches 32; Indels 51; Gaps 8;
QY 10 LRLVLGLWLLLRSVAGEQAGTAPCSRGSSWSADLDKCMDCASC-----RA 57
DB 104 LRAVLRAAFCLRLRAVAGARLVAAAP--EGAGLAAPQS--PAASCSANTSRSTFAPLRI 159

QY 58 RP-----HSDFCIGCA-AAPPAPFRLM-----PILGALSILTFVLGSLGFLV 100
Db 160 RPTFSPFRSRSCQAMASATPAPSATLWLVKRRMAPI---SLSLT----- 205
QY 101 WRRCRRERSPP 111
Db 206 -----RTRRSAP 212

RESULT 10

US-09-322-409-31
; Sequence 31, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-31

Query Match 12.6%; Score 76.5; DB 4; Length 250;
Best Local Similarity 27.5%; Pred. No. 0.95;
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

QY 11 RLVLGLWLLALRSVAG-----EQAPGTAPCSRGSWSA 44
Db 49 RLVLQQRWVRLQAVAGSQMQLLEAVNTEIHVTFCAFQDTSQQLAALKPWITRRNFSG 108
QY 45 DLD-KMDCASCARPHSDFCIGCAA--APPAPFRLMPLIGALSILTFVLGSLGFLV 101
Db 109 CLELQCPDSSTLVPRSPGALNTALPAQAP-RLLULLL---LPVALLMSTAWCLHW 164
QY 102 RRCRRERSPP 112
Db 165 RRRRRRSPP 175

RESULT 11

US-09-451-527-31
; Sequence 31, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 250
; TYPE: PRT

; ORGANISM: Canis familiaris
US-09-451-527-31

Query Match 12.6%; Score 76.5; DB 4; Length 250;
Best Local Similarity 27.5%; Pred. No. 0.95;
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

QY 11 RLVLGLWLLALRSVAG-----EQAPGTAPCSRGSWSA 44
Db 49 RLVLQQRWVRLQAVAGSQMQLLEAVNTEIHVTFCAFQDTSQQLAALKPWITRRNFSG 108
QY 45 DLD-KMDCASCARPHSDFCIGCAA--APPAPFRLMPLIGALSILTFVLGSLGFLV 101
Db 109 CLELQCPDSSTLVPRSPGALNTALPAQAP-RLLULLL---LPVALLMSTAWCLHW 164
QY 102 RRCRRERSPP 112
Db 165 RRRRRRSPP 175

RESULT 12

US-09-322-409-26
; Sequence 26, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;
Best Local Similarity 27.5%; Pred. No. 1.1;
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;

QY 11 RLVLGLWLLALRSVAG-----EQAPGTAPCSRGSWSA 44
Db 75 RLVLQQRWVRLQAVAGSQMQLLEAVNTEIHVTFCAFQDTSQQLAALKPWITRRNFSG 134
QY 45 DLD-KMDCASCARPHSDFCIGCAA--APPAPFRLMPLIGALSILTFVLGSLGFLV 101
Db 135 CLELQCPDSSTLVPRSPGALNTALPAQAP-RLLULLL---LPVALLMSTAWCLHW 190
QY 102 RRCRRERSPP 112
Db 191 RRRRRRSPP 201

RESULT 13

US-09-451-527-26
; Sequence 26, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2

; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 26
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-451-527-26

Query Match 12.6%; Score 76.5; DB 4; Length 276;
Best Local Similarity 27.5%; Pred. No. 1.1;
Matches 36; Conservative 15; Mismatches 47; Indels 33; Gaps 5;
QY 11 RLVGLWLLALLRSVAG-----EQAPGTAPCGRGSSWSA 44
Db 75 RLVLAQRWVRLQAVAGSQMILLEAVNTEHFVTFCAFDQTSQQLAALKPWITRRNFSG 134
QY 45 DLD-KMDCASCARPHSDFCGLCAA--APPAPRLLWPILGGALSLTFVLGLLGGFLVW 101
Db 135 CLELQCPDSDSTLVPPRSPGALEATALPAPQAP-RLLLLL---LPVALLMSTAWCLHW 190
QY 102 RRCRRERSPP 112
Db 191 RRRRRRSPYP 201

RESULT 14
US-09-252-991A-18795
; Sequence 18795, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18795
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18795

Query Match 12.3%; Score 75; DB 4; Length 334;
Best Local Similarity 35.6%; Pred. No. 1.9;
Matches 26; Conservative 7; Mismatches 30; Indels 10; Gaps 4;
QY 33 TAPCGSSWSADLDKCMDCASCARPHSDFCGLCAAAPPAPR--LLWPILGGALSLTF 90
Db 38 TTPTSTARSRPV-----APCLQAPAS--LLSTSTAPTATMAFDLNLALAG-LALAL 89
QY 91 VLGLLGGFLVWR 103
Db 90 VAGPLGSFVWR 102

RESULT 15
US-09-252-991A-21147
; Sequence 21147, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21147
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21147

Query Match 12.3%; Score 74.5; DB 4; Length 305;
Best Local Similarity 29.1%; Pred. No. 2;
Matches 37; Conservative 10; Mismatches 61; Indels 19; Gaps 4;
QY 3 RGSRLRLRLVLLGLWL---ALLRSVAGEQAPGTAPCGRGSSWSADLDKCMDCASCAR 58
Db 20 RPSTTRKPMCSLTLAESTAAVPSWACSESEPTLVMLRSMWATWLCSSAAVAICWL 79
QY 59 PHSDFCGLCA-----AAPAPRLLW-----PILGGALSLT-----FVLGLLGGFLVWR 103
Db 80 PSSSSTVATMRPSAWAALGASTLLWALPRMAATASLAPSCNGSINPWISWDCWVR 139
QY 104 CREERS 110
Db 140 LASERTS 146

Search completed: February 11, 2004, 10:40:26
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: February 11, 2004, 10:39:29 ; Search time 34 Seconds

(without alignments)
702.046 Million cell updates/sec

Title: US-10-062-599-59

Perfect score: 608

Sequence: 1 MARGSLRRLLRLVLGLWLA.....LSGLVWRRCRRRSPPPX 114

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Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	571	93.9	129	10	US-09-883-777-4
5	571	93.9	129	12	US-10-024-298A-178
6	571	93.9	129	12	US-10-042-211A-178
7	571	93.9	129	12	US-10-331-496A-37
8	571	93.9	129	12	US-10-295-027-444
9	571	93.9	129	12	US-10-295-027-1305
10	450	74.0	129	9	US-09-742-454A-5
11	450	74.0	129	10	US-09-883-777-5
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13	433	71.2	309	10	US-09-883-777-7
14	379.5	62.4	300	10	US-09-883-777-9
15	97.5	16.0	171	15	US-10-251-947-4

16 97.5 16.0 171 15 US-10-251-947-7
17 97.5 16.0 185 15 US-10-251-947-2
18 97.5 16.0 170 15 US-10-251-947-6
19 96.5 15.9 186 15 US-10-251-947-14
20 88.5 14.6 1307 15 US-10-303-685-17
21 88.5 14.6 1388 12 US-10-093-463-138
22 88.5 14.6 1388 12 US-10-093-463-140
23 87 14.3 184 15 US-10-008-063-2
24 87 14.3 184 15 US-10-152-363A-60
25 79.5 13.1 377 15 US-10-156-761-8962
26 76.5 12.6 270 12 US-10-262-439-31
27 76.5 12.6 250 15 US-10-218-654-31
28 76.5 12.6 276 12 US-10-262-439-26
29 76.5 12.6 276 15 US-10-218-654-26
30 76.5 12.6 732 15 US-10-156-761-12251
31 75.5 12.4 287 12 US-10-108-260A-3127
32 75.5 12.4 287 12 US-10-108-260A-3845
33 75.5 12.4 635 12 US-10-369-493-5911
34 75.5 12.4 635 12 US-10-369-493-5912
35 75 12.3 356 12 US-10-085-198-64
36 74 12.2 548 12 US-10-434-156-12
37 74 12.2 768 12 US-10-369-493-5165
38 73.5 12.1 187 11 US-09-975-719-287
39 73.5 12.1 409 15 US-10-156-761-11890
40 72.5 11.9 242 10 US-09-738-626-6004
41 72.5 11.9 365 11 US-09-860-836B-5
42 72.5 11.9 365 12 US-10-436-523-59
43 72.5 11.9 391 12 US-10-264-049-2579
44 72 11.8 257 12 US-10-104-047-3192
45 72 11.8 1278 15 US-10-208-731-2

ALIGNMENTS

RESULT 1
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens

Sequence 7, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 138, App
Sequence 140, App
Sequence 2, Appli
Sequence 60, Appli
Sequence 8962, Ap
Sequence 31, Appli
Sequence 31, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 12251, A
Sequence 3127, Ap
Sequence 3845, Ap
Sequence 5911, Ap
Sequence 5912, Ap
Sequence 12, Appli
Sequence 5165, Ap
Sequence 287, App
Sequence 11890, A
Sequence 6004, Ap
Sequence 5, Appli
Sequence 59, Appli
Sequence 2579, Ap
Sequence 3192, Ap
Sequence 2, Appli

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match      99.8%; Score 607; DB 12; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFLLWPIILGALLSLTFVLGSLGFLVWRCRRERSPPPP 113
Db 61 SDFCLGCAAAAPPAPFLLWPIILGALLSLTFVLGSLGFLVWRCRRERSPPPP 113

RESULT 2
US-10-062-831-59
; Sequence 59, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,831
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match      99.8%; Score 607; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFLLWPIILGALLSLTFVLGSLGFLVWRCRRERSPPPP 113

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96

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Db 61 SDFCLGCAAAAPPAPFLLWPIILGALLSLTFVLGSLGFLVWRCRRERSPPPP 113

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-742-454A-4

Query Match      93.9%; Score 571; DB 9; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFLLWPIILGALLSLTFVLGSLGFLVWRCRRERSPPPP 113
Db 61 SDFCLGCAAAAPPAPFLLWPIILGALLSLTFVLGSLGFLVWRCRREREFTTP 113

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-883-777-4

Query Match      93.9%; Score 571; DB 10; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db 1 MARGSLRLLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAAAPPAPFLLWPIILGALLSLTFVLGSLGFLVWRCRRERSPPPP 113

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Db 61 SDFCLGCAAPAPFRLWPIILGGALSLTFVLGSLGFLVWRCRRREKFTTP 113

RESULT 5

US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; PRIOR FILING DATE: 2003-04-08
; PRIOR FILING DATE: 2001-08-24, 395
; PRIOR FILING DATE: 2001-08-24, 641
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-178

Query Match 93.9%; Score 571; DB 12; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAPAPFRLWPIILGGALSLTFVLGSLGFLVWRCRRRSPP 113
Db 61 SDFCLGCAAPAPFRLWPIILGGALSLTFVLGSLGFLVWRCRRREKFTTP 113

RESULT 6

US-10-042-211A-178
; Sequence 178, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, AKIO et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; PRIOR FILING DATE: 2002-01-11
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2000-12-28
; PRIOR FILING DATE: 2001-08-24

Query Match 93.9%; Score 571; DB 12; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60

; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-178

Query Match 93.9%; Score 571; DB 12; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAPAPFRLWPIILGGALSLTFVLGSLGFLVWRCRRRSPP 113
Db 61 SDFCLGCAAPAPFRLWPIILGGALSLTFVLGSLGFLVWRCRRREKFTTP 113

RESULT 7

US-10-331-496A-37
; Sequence 37, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

FILE REFERENCE: P5014RI-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR FILING DATE: 2002-12-30
; PRIOR FILING DATE: 2002-01-02
; PRIOR FILING DATE: 2002-01-02
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2002-02-25
; PRIOR FILING DATE: 2002-02-25
; PRIOR FILING DATE: 2002-03-05
; PRIOR FILING DATE: 2002-03-05
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2002-03-21
; PRIOR FILING DATE: 2002-03-21
; PRIOR FILING DATE: 2002-03-28
; PRIOR FILING DATE: 2002-03-28
; PRIOR FILING DATE: 2002-08-19
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 37
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-37

Query Match 93.9%; Score 571; DB 12; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRRLRLVLLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKMDCASCRARPH 60

QY 61 SDFCLGCAAPPAPFRLWLPILGALSITFVLGSLGFLVWRRCRSSPPP 113
Db 61 SDFCLGCAAPPAPFRLWLPILGALSITFVLGSLGFLVWRRCRREKFTTP 113

RESULT 8

US-10-295-027-444
; Sequence 444, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444

Query Match 93.9%; Score 571; DB 12; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLLALLRSVAGEOAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEOAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAPPAPFRLWLPILGALSITFVLGSLGFLVWRRCRSSPPP 113
Db 61 SDFCLGCAAPPAPFRLWLPILGALSITFVLGSLGFLVWRRCRREKFTTP 113

RESULT 9

US-10-295-027-1305
; Sequence 1305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1305
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1305

Query Match 93.9%; Score 571; DB 12; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLLALLRSVAGEOAPGTAPCSRGSWSADLDKMDCASCRARPH 60
Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEOAPGTAPCSRGSWSADLDKMDCASCRARPH 60
QY 61 SDFCLGCAAPPAPFRLWLPILGALSITFVLGSLGFLVWRRCRSSPPP 113
Db 61 SDFCLGCAAPPAPFRLWLPILGALSITFVLGSLGFLVWRRCRREKFTTP 113

RESULT 10

US-09-742-454A-5
; Sequence 5, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5

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; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-742-454A-5

Query Match          74.0%; Score 450; DB 9; Length 129;
Best Local Similarity 75.2%; Pred. No. 3.2e-36;
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCCASCARPH 60
Db 1 MAPGWPRSLPQILVGLVGLVLMRAAGEQAPGTSPCSCSGSSWSADLDKMDCCASCARPH 60
QY 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRCRRERSPPP 113
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLVLLVLAIVSSFLVWRCRREREKFTTP 113

RESULT 11
US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match          74.0%; Score 450; DB 10; Length 129;
Best Local Similarity 75.2%; Pred. No. 3.2e-36;
Matches 85; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCCASCARPH 60
Db 1 MAPGWPRSLPQILVGLVGLVLMRAAGEQAPGTSPCSCSGSSWSADLDKMDCCASCARPH 60
QY 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRCRRERSPPP 113
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLVLLVLAIVSSFLVWRCRREREKFTTP 113

RESULT 12
US-09-742-454A-7
; Sequence 7, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.0
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; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
; OTHER INFORMATION: receptor fusion protein construct
US-09-742-454A-7

Query Match          71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.5e-34;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCCASCARPH 60
Db 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCCASCARPH 60
QY 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRCRRERSPPP 112
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLVLLVLAIVSSFLVWRCRREREKFTTP 90

RESULT 13
US-09-883-777-7
; Sequence 7, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7

Query Match          71.2%; Score 433; DB 10; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.5e-34;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCCASCARPH 60
Db 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKMDCCASCARPH 60
QY 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGLLSGFLVWRCRRERSPPP 112
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLVLLVLAIVSSFLVWRCRREREKFTTP 90

RESULT 14
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
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; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match 62.4%; Score 379.5; DB 10; Length 300;
Best Local Similarity 88.0%; Pred. No. 5.2e-29;
Matches 73; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MARGSLRLLRLVLGLWLLRLSRVAGEQAPCTAPCSRGSSWSADLDKCMDCASCRRPH 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MARGSLRLLRLVLGLWLLRLSRVAGEQAPCTAPCSRGSSWSADLDKCMDCASCRRPH 60

QY 61 SDFCLGCAAA-----PPAP 74
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 SDFCLGCAAAASCDKTHTCPCP 83

RESULT 15
US-10-251-947-4
; Sequence 4, Application US/10251947
; Publication No. US2003009990A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
; FILE REFERENCE: 01-1160-A
; CURRENT APPLICATION NUMBER: US/10/251,947
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-947-4

Query Match 16.0%; Score 97.5; DB 15; Length 171;
Best Local Similarity 31.8%; Pred. No. 0.069;
Matches 34; Conservative 9; Mismatches 39; Indels 25; Gaps 5;

QY 23 RSVAGEQAPCTAPCSRGSSWSADLDKCMDCASCRRPHSDFCLGCAAPAPFLLMP-- 80
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
6 RSLGRDAPVPTCPVTECDLLVRKVCDCRLRKSPK---TAAGASSPAPGTALQPQE 62

QY 81 -----ILGGA---LSLTFVLGL-LSGFLVWRCRRR 108
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
63 SVGTGSGEVSILPLPGLLFGAPALLGLVILVILVGLVSWRR-RQOR 108

Search completed: February 11, 2004, 10:44:55
Job time : 35 secs